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OM protein - protein search, using sw model

Run On: October 18, 2002, 10:33:53 ; Search time 13 Seconds

319.412 Million cell updates/sec  
(without alignments)

Title: US-09-218-913d-52

Perfect score: 948

Sequence: 1 ADRRS1HDFCLVSKVVGRC.....ACMLRCFRQQENPPLPLGSK 170

Scoring table: BLOSUM62

Gapext 0.5

Sequences: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/\_ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/\_ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/\_ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/\_ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/\_ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/\_ptodata/1/iaa/backfiles/pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	ID	Description
1	948	100.0	252	1	US-08-885-660A-7		Sequence 7, Appli
2	948	100.0	252	2	US-08-974-196-7		Sequence 7, Appli
3	948	100.0	252	4	US-09-071-709-10		Sequence 10, Appli
4	948	100.0	252	4	US-09-013-896A-2		Sequence 2, Appli
5	312	32.9	513	4	US-08-685-538A-18		Sequence 18, Appli
6	239.5	31.6	348	4	US-09-071-709-2		Sequence 2, Appli
7	297	31.3	51	4	US-09-013-896A-10		Sequence 10, Appli
8	297	31.3	51	4	US-09-013-896A-11		Sequence 11, Appli
9	247.5	26.1	122	2	US-08-122-333-12		Sequence 12, Appli
10	247.5	26.1	122	6	5187153-20		Patent No. 5187153
11	247.5	26.1	122	6	5220013-23		Patent No. 5220013
12	244.5	25.8	143	2	US-08-122-333-10		Sequence 10, Appli
13	244.5	25.8	143	6	5223482-20		Patent No. 5223482
14	244.5	25.8	144	6	5187153-18		Patent No. 5187153
15	243.5	25.8	147	1	US-08-158-160-72		Sequence 72, Appli
16	243.5	25.7	127	6	5466783-24		Patent No. 5466783
17	241.5	25.5	123	6	5466783-21		Patent No. 5466783
18	233.5	24.6	122	6	5223482-22		Patent No. 5223482
19	233.5	24.6	276	1	US-07-828-920A-1		Sequence 1, Appli
20	233.5	24.6	276	1	US-08-437-841-9		Sequence 9, Appli
21	233.5	24.6	276	1	US-08-386-521-9		Sequence 9, Appli
22	233.5	24.6	276	1	US-08-175-9		Sequence 9, Appli
23	233.5	24.6	276	1	US-08-796-850-1		Sequence 1, Appli
24	233.5	24.6	276	3	US-08-954-764-3		Sequence 3, Appli
25	233.5	24.6	276	4	US-08-943-652-9		Sequence 9, Appli
26	233.5	24.6	276	5	PCT-US95-09377-3		Sequence 3, Appli
27	233.5	24.6	276	5	PCT-US95-09464-9		Sequence 9, Appli

#### ALIGNMENTS

RESULT 1  
US-08-685-660A-7

; Sequence 7, Application US/08685660A  
; Patent No. 5731412

; GENERAL INFORMATION:  
; APPLICANT: SHIMOMURA, Takeshi  
; APPLICANT: KAWAGUCHI, Toshiya  
; APPLICANT: KITAMURA, Naomi  
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEES: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20037

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,660A  
; FILING DATE: 24-JUL-1996  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: JPA Hei 7-187134  
; APPLICATION NUMBER: JPA Hei 7-187134  
; FILING DATE: 24-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KIT, Gordon  
; REGISTRATION NUMBER: 30,764  
; RESEQUENCE/DOCKET NUMBER: Q-42295  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 293-7060  
; TELEFAX: (202) 293-7860  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 amino acids  
; TYPE: amino acid  
; MOLECULE: linear  
; MOLECULE TYPE: peptide  
; US-08-685-660A-7

Query Match 100.0%; Score 948; DB 1; Length 252;  
Best Local Similarity 100.0%; pred. No. 3.1e-92;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ADRESIHDCLVSKVGRASMRWWYNTDGSQLFYGGCDGNSNNLTKEECLKK 60  
|||||||

Db 28 ADRESRSHDFCLVSKVGRCRASMPWWVNTDGSCQLFVYGGCDGNSNNYLKEECLKK 87  
 Qy 61 CAVTENATGDLATSRNAADSSVPSAPRQDSEDHSSDMFNYEEYCTANAVTGPGRASFP 120  
 Db 88 CAVTENATGDLATSRNAADSSVPSAPRQDSEDHSSDMFNYEEYCTANAVTGPGRASFP 147  
 Db 121 RWYFDEVNCSNFIYGGCRGNKNSYRSEBACMLRCFQENPPLPLGSK 170  
 Db 148 RWYFDEVNCSNFIYGGCRGNKNSYRSEBACMLRCFQENPPLPLGSK 197

RESULT 2  
 US-08-974-196-7

; Sequence 7, Application US/0894196  
 ; Patent No. 5844396  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHIMOMURA, Takeshi  
 ; ADDRESS: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
 ; STREET: 2100 Pennsylvania Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20037

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/974,196  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/685,660  
 FILING DATE: 24-JUL-1996  
 APPLICATION NUMBER: JPA Hei 7-187134  
 FILING DATE: 24-JUL-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KIT, Gordon  
 REGISTRATION NUMBER: 30,764

REFERENCE DOCKET NUMBER: Q-4-2295  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 293-7060  
 TELEFAX: (202) 293-7860  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 252 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

US-08-974-196-7

Query Match 100.0%; Score 948; DB 4; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-92;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFE QUERY 1 ADRESRSHDFCLVSKVGRCRASMPWWVNTDGSCQLFVYGGCDGNSNNYLKEECLKK 60  
 DB 28 ADRESRSHDFCLVSKVGRCRASMPWWVNTDGSCQLFVYGGCDGNSNNYLKEECLKK 87

Qy 61 CAVTENATGDLATSRNAADSSVPSAPRQDSEDHSSDMFNYEEYCTANAVTGPGRASFP 120  
 Db 88 CAVTENATGDLATSRNAADSSVPSAPRQDSEDHSSDMFNYEEYCTANAVTGPGRASFP 147

Qy 121 RWYFDEVNCSNFIYGGCRGNKNSYRSEBACMLRCFQENPPLPLGSK 170  
 Db 148 RWYFDEVNCSNFIYGGCRGNKNSYRSEBACMLRCFQENPPLPLGSK 197

RESULT 3  
 US-09-071-709-10

; Sequence 10, Application US/09071709  
 ; Patent No. 6171790  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hallman, Jennifer L.  
 ; ADDRESS: 1000 NEW YORK AVE., NW, STE. 600  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/071,709  
 FILING DATE: Filed Herewith  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CERONE, Michael C.  
 REGISTRATION NUMBER: 39,132  
 REFERENCE/DOCKET NUMBER: PF-0513 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 855-0555  
 TELEFAX: (650) 845-4166  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 252 amino acids  
 TYPE: amino acid  
 STANDINGNESS: single  
 TOPOLOGY: linear

US-09-071-709-10

Query Match 100.0%; Score 948; DB 4; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-92;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADRESRSHDFCLVSKVGRCRASMPWWVNTDGSCQLFVYGGCDGNSNNYLKEECLKK 60  
 Db 28 ADRESRSHDFCLVSKVGRCRASMPWWVNTDGSCQLFVYGGCDGNSNNYLKEECLKK 87

Qy 61 CAVTENATGDLATSRNAADSSVPSAPRQDSEDHSSDMFNYEEYCTANAVTGPGRASFP 120  
 Db 88 CAVTENATGDLATSRNAADSSVPSAPRQDSEDHSSDMFNYEEYCTANAVTGPGRASFP 147

Qy 121 RWYFDEVNCSNFIYGGCRGNKNSYRSEBACMLRCFQENPPLPLGSK 170  
 Db 148 RWYFDEVNCSNFIYGGCRGNKNSYRSEBACMLRCFQENPPLPLGSK 197

RESULT 4  
 US-09-013-896A-2

; Sequence 2, Application US/09013896A  
 ; Patent No. 6262233  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GENTZ, REINER  
 ; TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: STEIN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 ; STREET: 1100 NEW YORK AVE., NW, STE. 600

CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: US  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/013,896A  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K.  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.1290001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8439  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 252 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-013-896A-2

Query Match 100.0%; Score 948; DB 4; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-12;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVYGRCRASMPRWWYNTDGSCOLFYGGCDGNSNNYLTKEECLKK 60  
 DB 28 ADERSIHDFCLVSKVYGRCRASMPRWWYNTDGSCOLFYGGCDGNSNNYLTKEECLKK 87

QY 61 CATVTEENATGDLATSRNAADSSVPSPAPRQDSEHSSDMFNEYCTANAVTGPCRASF 120  
 DB 88 CATVTEENATGDLATSRNAADSSVPSPAPRQDSEHSSDMFNEYCTANAVTGPCRASF 147

QY 121 RWFYDVERNSCNINFYGGCRGNKNSYRSEACMLRCRQENPPLGSK 170  
 DB 148 RWFYDVERNSCNINFYGGCRGNKNSYRSEACMLRCRQENPPLGSK 197

RESULT 5  
 US-08-085-558A-18  
 Sequence 18, Application US/08685558A  
 Patent No. 6225081  
 GENERAL INFORMATION:  
 APPLICANT: SHIMOMURA, Takeshi  
 APPLICANT: KAWAUCHI, Naomii  
 APPLICANT: MIYAWAWA, Keiji  
 TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
 NUMBER OF SEQUENCES: 18  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSSEE: SUCHRUE, MION, ZINN, MACPEAK & SEAS  
 STREET: 2100 Pennsylvania Avenue, N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20037

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy Disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/685,558A  
 FILING DATE: 24-JUL-1996  
 PRIORITY APPLICATION DATA:

APPLICATION NUMBER: JPA\_Hei 7-187135  
 FILING DATE: 24-JUL-1995  
 INFORMATION FOR SEQ ID NO: 18:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 513 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 STRAIN: MN45  
 US-08-085-558A-18

Query Match 32.9%; Score 312; DB 4; Length 513;  
 Best Local Similarity 33.5%; Pred. No. 7.6e-25;  
 Matches 67; Conservative 24; Mismatches 71; Indels 38; Gaps 5;

QY 5 RSIHDDFCLVSKVYGRCRASMPRWWYNTDGSCOLFYGGCDGNSNNYLTKEECLKKAT 64  
 DB 244 KOTEDCLASNYVGRGRCRGSFPRWVYPTEQICKSFYVGCLGKNNYLRPEECILACRGV 303

QY 65 -----TENATGDLATSRNAADS----SVPSAPRQDSD----EDHSSDMFNY 102  
 DB 304 QGPSPMERRHPVCSGTCOPTQFRCNSNGCCIDSFLECDTTPNCPDASDEAACYTKSGFDEL 363

QY 103 EB-----YCTANAVTGPCRASFPRWYFDEVNSCNINFYGGCRGNKNSYRSEPACML 154  
 DB 364 QRIHFPSDKGHCVLDPLGKESIPRWWYHNPFSEHARFTYGGCYGNKNNFEEOQCLE 423

RESULT 6  
 US-09-071-709-2  
 Sequence 2, Application US/09071709  
 Patent No. 6171790  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Tang, Y. Tom  
 APPLICANT: Lal, Preeti  
 APPLICANT: Corley, Neil C.  
 APPLICANT: Guegler, Karl J.  
 APPLICANT: Patterson, Chandra  
 TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 STREET: 3174 PORTER DRIVE  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/071,709  
 FILING DATE: Filed Herewith  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CERONE, MICHAEL C.  
 REGISTRATION NUMBER: 39,132  
 REFERENCE/DOCKET NUMBER: PF-0513 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 855-0555  
 TELEFAX: (650) 845-4166  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:



COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION NUMBER: US/08/422,333  
 FILING DATE: 13-APR-1995  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Shearer, Peter R.  
 REFERENCE/DOCKET NUMBER: 28-117  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 966-2438  
 FAX: (415) 968-2438  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 122 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-422-333-12

Query Match 26.1%; Score 247.5; DB 2; Length 122;  
 Best Local Similarity 32.4%; Pred. No. 7.5e-19;  
 Matches 48; Conservative 16; Mismatches 45; Indels 39; Gaps 1;

Qy 9 DFLCLSKVVGCRASMRPWWYNTDGSQCLFWYGGDGNSNNYLTKEECLKKCATVTEA 68  
 Db 3 DSCQDYSQGPCLGLFKRYFNGTSNACETFLYGGCMGNLNLSQECLOTCRTV--- 58

Qy 69 TGDLATSRNAADSSVPSAPRQDSEDHSMDMFNEYEYCTANAVTGPCRASPRWYFVER 128  
 Db 59 ---; Score 247.5; DB 2; Length 122;  
 Best Local Similarity 32.4%; Pred. No. 7.5e-19;  
 Matches 48; Conservative 16; Mismatches 45; Indels 39; Gaps 1;

Qy 129 NSCNNFETYGGCRGKNSYRSEACMLRC 156  
 Db 84 GKCVRFSYGGCKGNGNFKYSOKECKEYC 111

RESULT 10  
 5.187153-20  
 ; Patent No. 5187153  
 ; APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO  
 ; TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S  
 ; AMYLOID POLYPEPTIDE DERIVATIVES  
 ; NUMBER OF SEQUENCES: 33  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/502,273  
 ; FILING DATE: 29-MAR-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 361,912  
 ; FILING DATE: 06-JUN-1989  
 ; APPLICATION NUMBER: 359,911  
 ; FILING DATE: 12-MAY-1989  
 ; APPLICATION NUMBER: 87,002  
 ; FILING DATE: 18-AUG-1987  
 ; APPLICATION NUMBER: 8,810  
 ; FILING DATE: 30-JAN-1987  
 ; APPLICATION NUMBER: 948,376  
 ; FILING DATE: 31-DEC-1986  
 ; APPLICATION NUMBER: 932,193  
 ; FILING DATE: 17-NOV-1986  
 ; SEQ ID NO:20;  
 ; LENGTH: 122

Query Match 26.1%; Score 247.5; DB 6; Length 122;  
 Best Local Similarity 32.4%; Pred. No. 7.5e-19;  
 Matches 48; Conservative 16; Mismatches 45; Indels 39; Gaps 1;

Qy 129 NSCNNFETYGGCRGKNSYRSEACMLRC 156  
 Db 84 GKCVRFSYGGCKGNGNFKYSOKECKEYC 111

RESULT 12  
 US-08-422-333-10  
 ; Sequence 10, Application US/08422333  
 ; Patent No. 5912410  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CORDELL, Barbara L.  
 ; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE  
 ; NUMBER OF SEQUENCES: 30  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Scios, Inc.  
 ; STREET: 2450 Bayshore Parkway  
 ; CITY: Mountain View  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94043  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: FLOPPY disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/422,333

FILING DATE: 13-APR-1995  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Shearer, Peter R.  
 REGISTRATION NUMBER: 28-117  
 REFERENCE/DOCKET NUMBER: 21900-28048.00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 968-2438  
 INFORMATION FOR SEQ ID NO: 10:  
 LENGTH: 143 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-422-333-10

Query Match 25.8%; Score 244.5; DB 2; Length 143;  
 Best Local Similarity 31.8%; Pred. No. 1.9e-18; Indels 39; Gaps 1;  
 Matches 47; Conservative 15; Mismatches 47; Application Number: US-08-422-333-10

Qy 9 DFLCLSKVKGCRASMRMWWYNTDGSQCLFLVGGCGDGNSSNNYLKEECLKKCATVTEA 68  
 Db 24 DSCQLGYSAGPQMGMTMTRYNTSWACETFYQGGCGMGNNGNFEVTEKECLQTCRTVAA-- 81

Qy 69 TGDLATSRNAADSSVSPSAPRQDSEDHSSDMNYYEYCTANAVTGPORASPRWYFDVER 128  
 Db 82 -----

Qy 129 NSCNNFTYGGCRGNKNSYRSEACMLRC 156  
 Db 105 GKCVLFPYGGCGQGNKFSKECREYC 132

RESULT 13  
 5223482-20  
 ; Patent No. 5223482  
 ; APPLICANT: SCHILLING, JAMES W.; PONTE, PHYLLIS A.; CORDELL, BARBARA  
 ; TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE  
 ; NUMBER OF SEQUENCES: 34  
 ; INHIBITOR AMYLOID PROTEIN AND METHOD OF USE  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US-07/361,911  
 ; FILING DATE: 06-JUN-1989  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 359,911  
 ; FILING DATE: 12-MAY-1989  
 ; APPLICATION NUMBER: 87,002  
 ; FILING DATE: 18-AUG-1987  
 ; APPLICATION NUMBER: 948,376  
 ; FILING DATE: 31-DEC-1986  
 ; APPLICATION NUMBER: 932,193  
 ; FILING DATE: 17-NOV-1986  
 ; SEQ ID NO:20;  
 ; LENGTH: 143

5187153-18

Query Match 25.8%; Score 244.5; DB 6; Length 144;  
 Best Local Similarity 31.8%; Pred. No. 1.9e-18;  
 Matches 47; Conservative 15; Mismatches 47; Indels 39; Gaps 1;

Qy 9 DFLCLSKVKGCRASMRMWWYNTDGSQCLFLVGGCGDGNSSNNYLKEECLKKCATVTEA 68  
 Db 24 DSCQLGYSAGPQMGMTSRYTFNGTSWACETFYQGGCGMGNNGNFEVTEKECLQTCRTVAA-- 81

Qy 69 TGDLATSRNAADSSVSPSAPRQDSEDHSSDMNYYEYCTANAVTGPORASPRWYFDVER 128  
 Db 82 -----

Qy 129 NSCNNFTYGGCRGNKNSYRSEACMLRC 156  
 Db 105 GKCVLFPYGGCGQGNKFSKECREYC 132

RESULT 15  
 US-08-358-160-72  
 ; Sequence 72; Application US/08358160  
 ; Patent No. 5653143  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LEY, Arthur C.  
 ; APPLICANT: LADNER, Robert C.  
 ; APPLICANT: GUTERMAN, Sonia K.  
 ; APPLICANT: ROBERTS, Bruce L.  
 ; APPLICANT: MARYLAND, William  
 ; APPLICANT: KENT, Rachel B.  
 ; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ  
 ; NUMBER OF SEQUENCES: 234  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W. Suite 300  
 ; CITY: Washington  
 ; STATE: District of Columbia  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 25.8%; Score 244.5; DB 6; Length 143;  
 Best Local Similarity 31.8%; Pred. No. 1.9e-18; Indels 39; Gaps 1;  
 Matches 47; Conservative 15; Mismatches 47; Application Number: US-08-358-160-72

Qy 9 DFLCLSKVKGCRASMRMWWYNTDGSQCLFLVGGCGDGNSSNNYLKEECLKKCATVTEA 68  
 Db 24 DSCQLGYSAGPQMGMTSRYTFNGTSWACETFYQGGCGMGNNGNFEVTEKECLQTCRTVAA-- 81

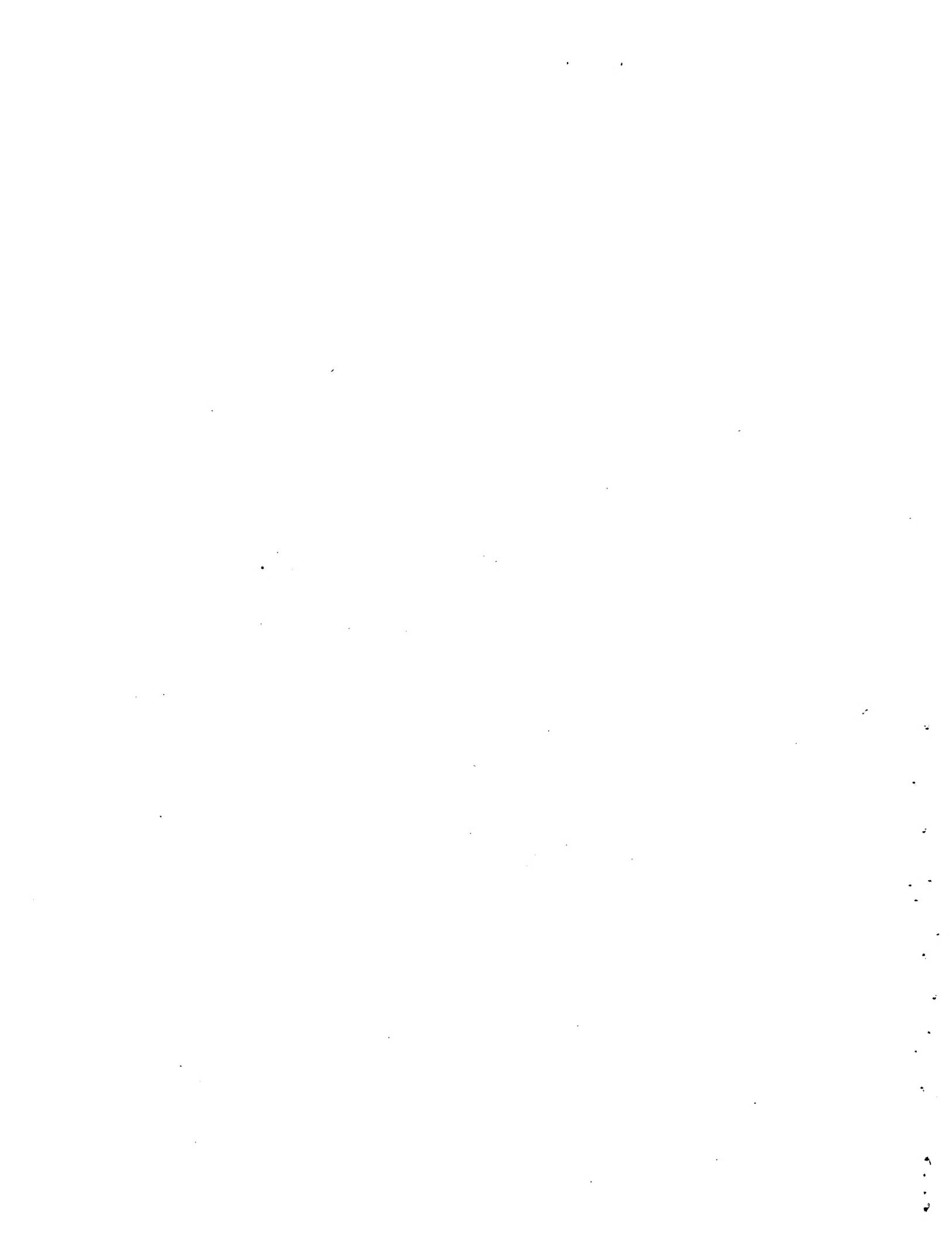
Qy 69 TGDLATSRNAADSSVSPSAPRQDSEDHSSDMNYYEYCTANAVTGPORASPRWYFDVER 128  
 Db 82 -----

Qy 129 NSCNNFTYGGCRGNKNSYRSEACMLRC 156

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/358,160  
FILING DATE: 16-DEC-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,031  
FILING DATE: 13-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/009,319  
FILING DATE: 26-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/664,989  
FILING DATE: 01-MAR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/487,063  
FILING DATE: 02-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/240,160  
FILING DATE: 02-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Cooper, Iver P.  
REGISTRATION NUMBER: 28,005  
REFERENCE DOCKET NUMBER: LEY-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 147 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

Query	Match	25.8%	Score	244.5	DB	1;	Length	147;
Best Local	Similarity	32.4%	Pred. No.	2e-18;				
Matches	48;	Conservative	14;	Mismatches	47;	Indels	39;	Gaps
Y	9	DFCLVSKVYGRCRASMPRWYNTDGSSQLFYGGCDNSNNYLTKECLLKRCATVTEA						68
Y	1	:						
D	24	DSCQGYSAGPCMGMTSRYFYNTGSMACTFQYGGCMNGNNFVTEKECLQTCRTVAA-						81
Y	69	TGDLATSRNAADSSVPSAARRDSDHSSDMFNEYEYCTANAVTGPCRASEPFWYDFVER						128
Y	82	-----						
C								
Y	129	NSCNNFIYGGCRONKNSYRSEEACMRLC						156

Search completed: October 18, 2002, 10:36:06  
Search time: 15 secs



Result No.	Score	Query	Match	Length	DB	ID	Description
1	948	100.0	252	4	Q969E0		Q969E0 homo sapien
2	381	40.2	195	11	Q9DB808		Q9dbq8 mus musculu
3	294	31.0	507	11	Q9D3K4		Q9d3k4 mus musculu
4	294	31.0	507	11	Q9J704		Q9j704 mus musculu
5	259	27.3	3060	5	Q9VAV4		Q9vav4 dirosophila
6	256	27.1	1572	5	Q44938		Q44938 haemöncophila
7	255	26.9	3198	5	Q9U8G8		Q9u8g8 manduca sex
8	252	26.6	287	13	Q93424		Q93424 cyprinus ca
9	250	26.4	2167	5	Q76840		Q76840 caenorhabdi
10	250	26.4	2174	5	Q9GQR0		Q9gqr0 dirosophila
11	244	25.8	151	4	P78491		P78491 homo sapien
12	240	25.3	2225	5	Q45881		Q45881 caenorhabdi
13	239	25.3	396	6	Q28874		Q28874 canis famili
14	235	24.8	349	11	Q9DBJ9		Q9dbj9 mus musculu
15	235	24.8	349	11	Q925W1		Q925w1 mus musculu
16	233	24.5	352	11	Q70160		Q70160 canis famili

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is denoted by a value of  $b$  in the formula  $b = \frac{1}{2} \ln \frac{1}{1 - \frac{1}{n}}$ .





Query Match 27.3%; Score 259; DB 5; Length 3060;  
 Best Local Similarity 32.9%; Pred. No. 2.5e-18;  
 Matches 52; Conservative 16; Mismatches 66; Indels 24; Gaps . 3;

Qy 9 DIFCQVSKVYGRCRASMPRWNWNTDGSCOLFYGGCDGNSNNYLTKEECLKKCATVTENA 68  
 Db 1807 DICEIPAEGCANEVTSWYQTDQACRFQYGGCGNENRFPTTEESCLARCDRKPEPT 1866

Qy 69 TGDLATSRNAAASSVSPAPRQDSEHDSSDMNYYEYCTANVTGPOASFRPWYDVER 128  
 Db 1867 TTTPATR-----PQPSRQD-----VCDEEAPGECSTWIKWHDTRKI 1904

Qy 129 NSCENNFIYGGCRNKNSYRSEACMLRCFQEQNPLP 166  
 Db 1905 GACRQFYGYGNCGGNGNRFETENDCQQRQLSQE--PPAP 1940

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RESULT 6

044938 PRELIMINARY; PRT; 1572 AA.  
 AC 044938; PRELIMINARY;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE TIRMBOSPONDIN.  
 GN TIRL.  
 OS Haemonchus contortus.  
 OC Nematoda; Chromadorea; Rhabditida; Strongylida;  
 OC Trichoscyrrhynyoidea; Haemonchidae; Haemonchus.  
 OX NCBI\_TAXID=6289;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPRAINMOREDUN;  
 RA Skuce P.J., Newlands G.F.J., Stewart M., Pettit D., Smith D.,  
 RA Knox D.P.;  
 RT "Cloning and characterization of thrombospondin, a novel multidomain  
 glycoprotein associated with the gut of Haemonchus contortus.";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF043121; AAB99830.2;  
 DR HSSP; P00506; 1CAU;  
 DR InterPro; IPR000361; EGF-like;  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR InterPro; IPR000384; TSPI.  
 DR InterPro; IPR0014; Kunitz\_BPTI;  
 DR PFM; P000050; TSPI\_1;  
 DR PROSITE; PS00759; BASICPTASE.  
 DR SMART; SM00131; KU\_6;  
 DR SMART; SM00001; EGF-like; 1.  
 DR PROSITE; PS00092; TSPI\_2.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2;  
 DR PROSITE; PS500280; BPTI\_KUNITZ\_1;  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2;  
 DR PROSITE; PS50092; TSPI\_1.  
 KW Immunoglobulin domain; Serine protease inhibitor; Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 SQ SEQUENCE 3198 AA; 349364 MW; ABACD459C0D9134 CRC64;

Query Match 26.9%; Score 255; DB 5; Length 3198;  
 Best Local Similarity 31.7%; Pred. No. 6.9e-18;  
 Matches 51; Conservative 23; Mismatches 63; Indels 24; Gaps 3;

Qy 9 DFCCLVSKVYGRCRASMPRWNWNTDGSCOLFYGGCDGNSNNYLTKEECLKKCATVTENA 68  
 Db 213.3 DLCTLPAAIGDCADYERWYDTRERSCQRFYGGCAGNGNNFATQAECEGRC----- 2185

Qy 69 TGDLATSRNAAASSVSPAPRQDSEHDSSDMNYYEYCTANVTGPOASFRPWYDVER 128  
 Db 218.6 -----SEAKITTVR--PTEAHP----LTENCFMEKDPGPCTDTETRWYDYL 2228

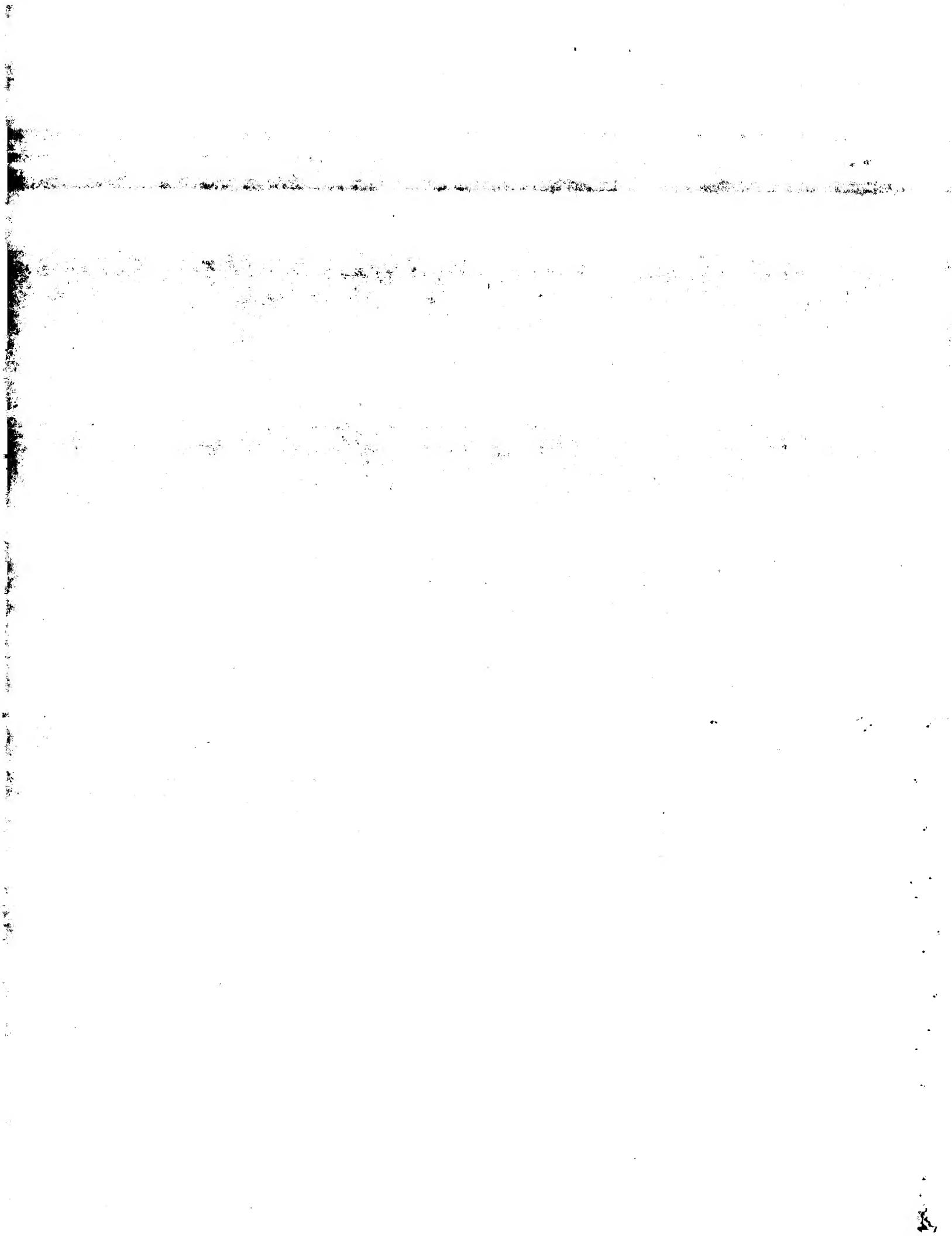
RESULT 8

033424 PRELIMINARY; PRT; 287 AA.  
 ID 033424; PRELIMINARY;  
 AC 033424; PRELIMINARY;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL 33.1 KDa PROTEIN.  
 OS Cyprinus carpio (Common carp).  
 OC Eukaryota; Metazoa; Chordata; Tracheata; Hexapoda; Lepidoptera; Giossata; Diptysia;  
 OC Spingiidae; Sphingidae; Neopterygii; Teleostei; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi;



Query Match	26.4%	Score 250;	DB 5;	Length 2174;				
Best Local Similarity	31.5%	Pred. No. 1.5e-17;						
Matches	46;	Conservative	20;	Mismatches	44;	Indels	36;	Gaps 2;
NCBI_TAXID	9121454;	SEQUENCE FROM N.A.						
QY	11	CLVSYVGRCRASMPRWNNTGDSCOLFVYGGDGNNSNNYLKECLKKCAYTENA 70						
Db	1671	CLLPKSAGPCTFTKWWFDDVRNRCFEFYQGCGTNNRDSLBCQGTC----- 1721						
QY	71	DLATSRNAADSSVPSAPRQDSEDHSSDMFNEYEYCTANAVYGPGRASFPRWYFDEVERNS 130						
Db	1722	-----AASENLPT-----CEQPVSESGPCAGNFERWYDNETDI 1754						
QY	131	CNNFIYGGCRGNKNSYKSEBACMLRC 156						
Db	1755	CRPETYSGCKGNKNNPTEHAGNYNC 1780						
RESULT 11								
P78491		PRELIMINARY;		PRT;	151 AA.			
AC	P78491;							
DT	01-MAY-1997	(TREMBLrel. 03, Created)						
DT	01-MAY-1997	(TREMBLrel. 03, Last sequence update)						
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)						
DE	ALPHA-1-MICROGLOBULIN (FRAGMENT).							
OS	Homo sapiens (Human).							
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;							
NCBI_TAXID	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
RN	11	SEQUENCE FROM N.A.						
RP	MEDLINE-9121454;	PubMed=1708673;						
RX	Yetr H., Gebhard W.;	"Structure of the human alpha-1-microglobulin gene."						
RX	BLIOL. Chem. Hoppe-Seyler 371:1185-1196 (1990).							
DR	Y54818;	CA38587.1;						
DR	HSSP; P02760;	1BVK.						
DR	InterPro; IPR00223;	Kunitz_BPTI.						
DR	PRINTS; PRO0014;	Kunitz_BPTI; 2.						
DR	PRINTS; PRO00759;	BASICPTASE.						
DR	SMART; SM00131;	KU; 2.						
DR	PROSITE; PS00280;	BPTI_KUNITZ_1;						
DR	PROSITE; PS00484;	THYROGLOBULIN_1;						
KW	Serine protease inhibitor.							
SQ	SEQUENCE 151 AA;	16542 MW;	88F400C5EA19831 CRC64;					
QY	9	DECLVSYVGRCRASMPRWNNTGDSCOLFVYGGDGNNSNNYLKECLKKCAYTENA 68						
Db	28	DSCOLGTSAGPQMGMTSRYTSNMACETQYGGCGNGNFTVETEKECLQTCRTVAA -- 85						
QY	69	TGDLATSRNAADSSVPSAPRQDSEDHSSDMFNEYEYCTANAVTGPGRASFPRWYFDEVERNS 128						
Db	86	-----CNLPPIVRGPFCRAFTIQLWAFDAVK 108						
QY	129	NSCENNFIYGGCRGNKNSYRSEBACMLRC 156						
Db	109	GKCVLFPYGGCGNGNKFYSEKECREYC 136						
RESULT 12								
Q45881		PRELIMINARY;		PRT;	2225 AA.			
AC	Q45881;							
DT	01-JUN-1998	(TREMBLrel. 06, Created)						
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)						
DE	W01F3.3 PROTEIN.							
GN	W01F3.3.							
QY	1	SEQUENCE FROM N.A.						
Db	90	PRELIMINARY;		PRT;	396 AA.			
RX	MEDLINE-95071310;	PubMed=7980463;						
RA	Girard T.J., Gaihani D., Broze G.J.Jr.;							
RT	"Complementary DNA sequencing of canine tissue factor pathway inhibitor reveals a unique nonmeric repetitive sequence between the second and third Kunitz domains."							
RT	Bichem. J. 303:923-928 (1994).							
RL	EMBL; S75369; AAB32443.1; -.							
DR	HSSP; P10646; ITFX.							
DR	InterPro; IPR002223; Kunitz_BPTI.							
DR	PFam; PF00014; Kunitz_BPTI; 3.							





GenCore version 5.1.3  
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Om protein - protein search, using sw model

Run on: October 18, 2002, 10:33:48 ; Search time 12 Seconds

(without alignments)  
548.527 Million cell updates/sec

Title: US-09-218-913D-52

Perfect score: 948

Sequence: 1 ADRRS1HDFCLVSKVVGRC. .... . ACMRLRCFRQQENPPLPLGSK 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1052244 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 1052244

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40\_\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	948	100.0	252	1 SPT2_HUMAN	043291 homo sapien
2	663	69.9	252	1 SPT2_MOUSE	Q9w03 sus musculu
3	312	32.9	513	1 SPT1_HUMAN	Q3278 homo sapien
4	294	31.0	507	1 SPT1_MOUSE	Q9r097 mus musculu
5	259.5	27.4	306	1 TFP1_MOUSE	Q5b191 mus musculu
6	249.5	26.3	352	1 AMBP_BOVIN	P00978 bos taurus
7	247.5	26.1	346	1 AMBP_MERIN	Q62577 meriones un
8	246.5	26.0	302	1 TFP1_RAT	Q02445 rattus norv
9	244.5	25.8	123	1 IATR_SHEEP	P13371 ovis aries
10	244.5	25.8	352	1 AMBP_HUMAN	P02760 homo sapien
11	244	25.7	300	1 TFP1_RABIT	P19761 oryctolagus
12	242.5	25.6	337	1 AMBP_PIG	P04366 sus scrofa
13	241.5	25.5	123	1 IATR_HORSE	P04365 equus cabal
14	237.5	25.1	349	1 AMBP_RAT	Q6240 rattus norv
15	235.5	24.9	304	1 TFP1_MACMU	Q28864 macaca mulu
16	235.5	24.8	349	1 AMBP_MESAU	Q60559 mesoceretus
17	235.5	24.8	349	1 AMBP_MOUSE	Q07456 mus musculu
18	233.5	24.6	304	1 TFP1_HUMAN	P10646 homo sapien
19	214.5	22.6	235	1 TFP2_HUMAN	P48307 homo sapien
20	210	22.2	765	1 APP2_RAT	P15943 rattus norv
21	204.5	21.6	230	1 APP2_MOUSE	Q35536 mus musculu
22	200	21.1	763	1 APP2_HUMAN	P06481 homo sapien
23	191	20.1	1416	1 YN81_CAEEL	Q03610 caenorhabdi
24	18.5	19.8	770	1 A4_RAT	P08592 rattus norv
25	18.6	19.6	751	1 A4_SAISC	Q95241 saimiri sci
26	18.6	19.6	770	1 A4_HUMAN	P05067 homo sapien
27	18.5	19.4	770	1 A4_MOUSE	P12023 mus musculu
28	181.5	19.1	355	1 AMBP_PLFPL	P36992 pleuronectes
29	175.5	18.5	69	1 CRPT_BOONI	P81162 boophilus m
30	174.5	18.4	76	1 A4_MACMU	P29216 macaca mulu
31	174.5	18.4	87	1 A4_MACFEA	P53601 macaca fasc
32	171.5	18.1	197	1 MCP_MELOC	P82968 melithaea c
33	170	17.9	58	1 AXPL_ANTRAF	P81547 anthopleura

#### ALIGNMENTS

RESULT 1  
SPN2\_HUMAN STANDARD; PRT; 252 AA.

ID SPN2\_HUMAN STANDARD; PRT; 252 AA.  
AC 043291\_000271; O14895; Q969E0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Kunitz-type Protease inhibitor 2 precursor (Hepatocyte growth factor activator inhibitor type 2) (HAI-2) (Placental bikunin).

GN SPINT2 OR HAI2 OR KOP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI\_TaxID=9006; RN [11]

SEQUENCE FROM N.A.

RP MEDLINE=98010584; PubMed=9246890;

RA Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denda K., Kitamura N.;

RA "Purification and cloning of hepatocyte growth factor activator inhibitor type 2, a Kunitz-type serine protease inhibitor.";

RL J. Biol. Chem. 272:27558-27564 (1997).

RN (2)

RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.

RC TISSUE=Lacenta;

RC Marlor C.W., Delaria K.A., Muller D.K., Greve J.M., Tamburini P.P.;

RA "Identification and cloning of human placental bikunin, a novel serine protease inhibitor containing two Kunitz domains.";

RL J. Biol. Chem. 272:12208-12208 (1997).

RN (3)

RP SEQUENCE FROM N.A.

RC TISSUE=Pancreatic cancer.

RP MEDLINE=98094245; PubMed=9434156;

RA Buechler M., Adler G., Wallrapp C., Bartels K., Varga G., Friess H.,

RA "Cloning of a new Kunitz-type protease inhibitor with a putative transmembrane domain overexpressed in pancreatic cancer.";

RL J. Biolog. Biophys. Acta 1395:88-95 (1998).

RN (4)

RP SEQUENCE FROM N.A., AND VARIANT LEU-200.

RC TISSUE=Colon, and Ovary;

RC Strausberg R.;

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,

CC -1- PLASMA AND TISSUE KALLIKREIN, AND FACTOR XIA.

CC -1- SUBCELLULAR LOCATION: Type I membrane Protein (Potential).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,

CC -1- PROSTATE, TESTIS, THYMUS, AND TRACHEA.

CC -1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 BPT1/KUNITZ INHIBITOR DOMAINS.

CC -1- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,

CC -1- PLASMA AND TISSUE KALLIKREIN, AND FACTOR XIA.

CC -1- SUBCELLULAR LOCATION: Type I membrane Protein (Potential).

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CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,

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CC -1- SIMILARITY: CONTAINS 2 BPT1/KUNITZ INHIBITOR DOMAINS.

CC -1- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,

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CC -1- SUBCELLULAR LOCATION: Type I membrane Protein (Potential).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,

CC -1- PROSTATE, TESTIS, THYMUS, AND TRACHEA.

CC -1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 BPT1/KUNITZ INHIBITOR DOMAINS.

CC -1- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,

CC -1- PLASMA AND TISSUE KALLIKREIN, AND FACTOR XIA.

CC -1- SUBCELLULAR LOCATION: Type I membrane Protein (Potential).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,

CC -1- PROSTATE, TESTIS, THYMUS, AND TRACHEA.

CC -1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 BPT1/KUNITZ INHIBITOR DOMAINS.

CC -1- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,

CC -1- PLASMA AND TISSUE KALLIKREIN, AND FACTOR XIA.

CC -1- SUBCELLULAR LOCATION: Type I membrane Protein (Potential).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,

CC -1- PROSTATE, TESTIS, THYMUS, AND TRACHEA.

CC -1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 BPT1/KUNITZ INHIBITOR DOMAINS.

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CC -1- SUBCELLULAR LOCATION: Type I membrane Protein (Potential).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,

CC -1- PROSTATE, TESTIS, THYMUS, AND TRACHEA.

CC -1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.

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CC -1- PROSTATE, TESTIS, THYMUS, AND TRACHEA.

CC -1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 BPT1/KUNITZ INHIBITOR DOMAINS.

CC -1- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,

CC -1- PLASMA AND TISSUE KALLIKREIN, AND FACTOR XIA.

CC -1- SUBCELLULAR LOCATION: Type I membrane Protein (Potential).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,

CC -1- PROSTATE, TESTIS, THYMUS, AND TRACHEA.

CC -1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 BPT1/KUNITZ INHIBITOR DOMAINS.

CC -1- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,

CC -1- PLASMA AND TISSUE KALLIKREIN, AND FACTOR XIA.

CC -1- SUBCELLULAR LOCATION: Type I membrane Protein (Potential).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,

CC -1- PROSTATE, TESTIS, THYMUS, AND TRACHEA.

CC -1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.

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CC -1- PLASMA AND TISSUE KALLIKREIN, AND FACTOR XIA.

CC -1- SUBCELLULAR LOCATION: Type I membrane Protein (Potential).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,

CC -1- PROSTATE, TESTIS, THYMUS, AND TRACHEA.

CC -1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 BPT1/KUNITZ INHIBITOR DOMAINS.

CC -1- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,

CC -1- PLASMA AND TISSUE KALLIKREIN, AND FACTOR XIA.

CC -1- SUBCELLULAR LOCATION: Type I membrane Protein (

DE	activator inhibitor type 2	(HAI-2).
GN	SPINT2 OR HAI2.	
OS	Mus musculus (Mouse).	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC	NCBI_TAXID=10090;	
OC	[1]	
RN	RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.	
RC	STRAIN=BALB/C;	
RX	MEDLINE:99160423; PubMed=10049781;	
RA	Itoh H.; Kataoka H.; Hamasuna R.; Kitamura N.; Koono M.;	
RA	Hepatocyte growth factor activator inhibitor type 2 lacking the first	
RT	Kunitz-type serine proteinase inhibitor domain is a predominant	
RT	product in mouse but not in human <sup>n</sup> ;	
RT	Biochem. Biophys. Res. Commun. 255:740-748 (1999).	
RL		
CC	-!- FUNCTION: INHIBITOR OF HGF ACTIVATOR.	
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).	
CC	-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE	
CC	PRODUCED BY ALTERNATIVE SPLICING.	
CC	-!- TISSUE SPECIFICITY: ISOFORM 2 IS MORE PREDOMINANT EXPRESSED THAN	
CC	ISOFORM 1.	
CC	-!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITOR DOMAINS.	
CC	-!- SIMILARITY: CONTAINS 2 BPT1/KUNITZ INHIBITOR DOMAINS.	
CC	-	
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation	
CC	the European Bioinformatics Institute. There are no restrictions on	
CC	use by non profit institutions as long as its content is in no	
CC	modified and this statement is not removed. Usage by and for commercial	
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .	
CC	-	
CC	EMBL: AF0999016; AAD22172.1; -.	
DR	DR AF0999019; AAD22173.1; -.	
DR	DR AF0999020; AAD22174.1; -.	
DR	DR P05067; ITAW.	
DR	DR MGI:1338031; Sprint2.	
DR	DR InterPro; IPR002233; Kunitz_BPT1.	
DR	DR Pfam; PF00014; Kunitz_BPT1; 2.	
DR	DR PRINTS; PRO0759; BASIC_CPTASE.	
DR	SMART; SM00131; KU; 2.	
DR	PROSITE; PS00280; BPT1_KUNITZ_1; 2.	
DR	DR PS50279; BPT1_KUNITZ_2; 2.	
KW	Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane;	
KW	SIGNAL; Alternative splicing.	
FT	FT SIGNAL 1 27 POTENTIAL	
FT	FT CHAIN 28 252 KUNITZ-TYPE PROTEASE INHIBITOR 2.	
FT	FT DOMAIN 28 197 EXTRACELLULAR (POTENTIAL).	
FT	FT TRANSMEM 198 218 POTENTIAL.	
FT	FT DOMAIN 219 252 CYTOPLASMIC (POTENTIAL).	
FT	FT DOMAIN 38 88 BPT1/KUNITZ INHIBITOR 1.	
FT	FT DOMAIN 133 183 BPT1/KUNITZ INHIBITOR 2.	
FT	FT DISULFID 38 88 BY SIMILARITY.	
FT	FT CHAIN 28 252 BY SIMILARITY.	
FT	FT DOMAIN 63 84 BY SIMILARITY.	
FT	FT TRANSMEM 198 218 REACTIVE BOND (BY SIMILARITY).	
FT	FT ACT_SITE 48 49 BY SIMILARITY.	
FT	FT DISULFID 133 183 BY SIMILARITY.	
FT	FT DISULFID 142 166 BY SIMILARITY.	
FT	FT DISULFID 158 179 BY SIMILARITY.	
FT	FT DISULFID 47 71 BY SIMILARITY.	
FT	FT DISULFID 63 84 BY SIMILARITY.	
FT	FT ACT_SITE 143 144 REACTIVE BOND (BY SIMILARITY).	
FT	FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	FT VARSPLIC 37 93 MISSING (IN ISOFORM 2 AND ISOFORM 3).	
FT	FT VARSPLIC 114 128 PRKSAEADSAEIFN -> CFVEELSVAALEIFYA (IN ISOFORM 3).	
FT	FT VARSPLIC 129 252 MISSING (IN ISOFORM 3).	
FT	FT SEQUENCE 252 AA; 27914 MW; B2FF4B6924D4F8F CRC64;	
SQ	Query Match 69.9%; Score 663; DB 1; Length 252;	
Best Local Similarity 68.28%; Pred. No. 4.1e-56;		
Matches 116; Conservative 21; Mismatches 33; Indels 0; Gaps 1;		
1 ADPBP1TIDECLYKAVKCPGCPASMDPDTYNNNDGSCGDCNINVIVKPPCCTV		



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CC EMBL: AF09018; AAF02490; 1;  
 DR HSSP; P05067; 1TAW.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR InterPro; IPR002172; LDL\_recept\_A.  
 DR Pfam; PF00014; Kunitz\_BPTI; 2.  
 DR Pfam; PF00057; LDL\_recept\_a; 1.  
 DR PRINTS; PRO0759; BASICPTASE.  
 DR SMART; SM00131; KU; 2.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
 DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 2.  
 DR PROSITE; PS01209; LDlRA\_1; FALSE\_NEG.  
 DR PROSITE; PS50088; LDlRA\_2; 1.  
 KW Repeat; Glycoprotein; Signal.

FT SIGNAL 1 29 POTENTIAL.  
 FT CHAIN 30 507 KUNITZ-TYPE PROTEASE INHIBITOR 1.  
 FT DOMAIN 244 294 BPTI\_KUNITZ INHIBITOR 1.  
 FT DOMAIN 312 348 LDL-RECEPTOR CLASS A.  
 FT DOMAIN 369 419 BPTI\_KUNITZ INHIBITOR 2.  
 FT DISULFID 244 294 BY SIMILARITY.  
 FT DISULFID 253 277 BY SIMILARITY.  
 FT DISULFID 269 290 BY SIMILARITY.  
 FT ACT-SITE 254 255 REACTIVE BOND (BY SIMILARITY).  
 FT DISULFID 369 419 BY SIMILARITY.  
 FT DISULFID 378 402 BY SIMILARITY.  
 FT DISULFID 394 415 BY SIMILARITY.  
 FT ACT-SITE 379 380 REACTIVE BOND (BY SIMILARITY).  
 FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 507 AA; 56676 MW; 20C5DEDCEF46AA7 CRC64;

Query Match 59; Conservative 31.0%; Score 294; DB 1; Length 507;  
 Best Local Similarity 33.1%; Pred. No. 1.2e-20; Gaps 3;  
 Matches 23; Mismatches 66; Indels 30; Gaps 3;

Qy 9 DFLCLVSKVYGRCRASMPRWYNTDGSQFLVYGGCGNSNNYLTKKECLLKCATV---- 64  
 Db 242 DYCLASYKVGRGSRFPRWYDPKEQICKSFTFGCLGNKNNYLREECMCLAKDVQGIS 301

Qy 65 -----TEAAGDGLATSRNAAD----SVPSPAPRQDSEDHSSDMNFYEE---- 104

Db 302 PRKRHPVCSSECSQHAFQRCNSGSDGFLRCDFDPGDSDEATCEKYTSGFDLQNIH 361

Qy 105 -----YCTANAVTGPGRASPRWYDFVERNSCNMFYGGCRGKNSYRSEACMLRC 156

Db 362 FLSDRGYCAELPDTGCKENIPRWWYNNPFSERCARFTYGGCGYGNKNNFEEOQCLES 419

RESULT 5  
 TFP1\_MOUSE  
 ID TFP1\_MOUSE  
 STANDARD; PRT; 306 AA.

AC 054819; O9Z2U8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-associated coagulation inhibitor) (LAC1) (Extrinsic pathway inhibitor (EPI).  
 GN TFP1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;

OX NCBI\_Taxid=10050;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA).

RC STRAIN=129;

MEDLINE=98152575; PubMed=9493581;

RX

RA Chang J.-Y., Monroe D.M., Oliver J.A., Liles D.K., Roberts H.R.;  
 CC "Cloning, expression, and characterization of mouse tissue factor  
 CC pathway inhibitor (TFPI)." RT  
 CC RT Thromb. Haemost. 79:306-309 (1998).  
 CC RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM BETA).  
 RX MEDLINE=99138770; PubMed=974373;  
 RA Chang J.-Y., Monroe D.M., Oliver J.A., Roberts H.R.;  
 RT "TFPIbeta, a second product from the mouse tissue factor pathway  
 RT inhibitor (TFPI) gene." RT  
 RL Thromb. Haemost. 81:45-49 (1999).  
 CC -|- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT  
 CC WAY, INHIBITS VII(A) TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING  
 CC A QUATERNARY X(A)/LAC1(VII(A))/TFI COMPLEX. IT POSSESSES AN  
 CC ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH  
 CC LIPOPROTEINS IN PLASMA (BY SIMILARITY).  
 CC -|- SUBCELLULAR LOCATION: 2 isoforms; alpha/TFPIalpha (shown here) and  
 CC beta/TFPIbeta; are produced by alternative splicing.  
 CC -|- TISSUE SPECIFICITY: Isoform alpha is expressed in heart and lung  
 CC spleen; isoform beta in heart and lung.  
 CC -|- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.  
 CC -|- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.  
 CC -|- DOMAIN: 300 507 BPTI/KUNITZ INHIBITOR 1.  
 CC -|- DOMAIN: 312 348 LDL-RECEPTOR CLASS A.  
 CC -|- DOMAIN: 369 419 BPTI/KUNITZ INHIBITOR 2.  
 CC -|- DISULFID 244 294 BY SIMILARITY.  
 CC -|- DISULFID 253 277 BY SIMILARITY.  
 CC -|- DISULFID 269 290 BY SIMILARITY.  
 CC -|- ACT-SITE 254 255 REACTIVE BOND (BY SIMILARITY).  
 CC -|- DISULFID 369 419 BY SIMILARITY.  
 CC -|- DISULFID 378 402 BY SIMILARITY.  
 CC -|- DISULFID 394 415 BY SIMILARITY.  
 CC -|- ACT-SITE 379 380 REACTIVE BOND (BY SIMILARITY).  
 CC -|- CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC -|- CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 507 AA; 56676 MW; 20C5DEDCEF46AA7 CRC64;

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CC -|- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.  
 CC -|- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.  
 CC -|- DOMAIN: 300 507 BPTI/KUNITZ INHIBITOR 1.  
 CC -|- DOMAIN: 312 348 LDL-RECEPTOR CLASS A.  
 CC -|- DOMAIN: 369 419 BPTI/KUNITZ INHIBITOR 2.  
 CC -|- DISULFID 244 294 BY SIMILARITY.  
 CC -|- DISULFID 253 277 BY SIMILARITY.  
 CC -|- DISULFID 269 290 BY SIMILARITY.  
 CC -|- ACT-SITE 254 255 REACTIVE BOND (BY SIMILARITY).  
 CC -|- DISULFID 369 419 BY SIMILARITY.  
 CC -|- DISULFID 378 402 BY SIMILARITY.  
 CC -|- DISULFID 394 415 BY SIMILARITY.  
 CC -|- ACT-SITE 379 380 REACTIVE BOND (BY SIMILARITY).  
 CC -|- CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC -|- CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 507 AA; 56676 MW; 20C5DEDCEF46AA7 CRC64;

DR EMBL; AE004833; AAC0035.1; DR EMBL; AE016313; AAC01586.1; DR HSSP; P10616; ITFX.  
 DR SMART; SM00131; KU; 3; DR PROSITE; PS00280; BPTI\_KUNITZ\_1; DR MGII; MGII:1095418; Tfp1.  
 DR InterPro; IPR002223; Kunitz\_BPTI. DR Pfam; PF00014; Kunitz\_BPTI; DR PRINTS; PR00159; BASICPTASE.  
 DR SMART; SM00131; KU; 3; DR PROSITE; PS50219; BPTI\_KUNITZ\_2; DR Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation; KW Signal; Alternative splicing. FT SIGNAL 1 28 BY SIMILARITY.  
 FT CHAIN 29 306 BPTI/KUNITZ INHIBITOR 1.  
 FT DOMAIN 50 100 (VII(A))/TISSUE FACTOR BINDING SITE).  
 FT DOMAIN 121 171 BPTI/KUNITZ INHIBITOR 2 (FACTOR VII(A) BINDING SITE).  
 FT DOMAIN 225 275 BPTI/KUNITZ INHIBITOR 3.  
 FT DOMAIN 29 306 BPTI/KUNITZ INHIBITOR 1.  
 FT DOMAIN 50 100 BY SIMILARITY.  
 FT DOMAIN 75 96 BY SIMILARITY.  
 FT ACT-SITE 60 61 REACTIVE BOND (BY SIMILARITY).  
 FT DISULFID 121 171 BY SIMILARITY.  
 FT DISULFID 130 154 BY SIMILARITY.  
 FT ACT-SITE 131 132 REACTIVE BOND (BY SIMILARITY).  
 FT DISULFID 225 275 BY SIMILARITY.  
 FT DISULFID 234 258 BY SIMILARITY.  
 FT ACT-SITE 250 271 BY SIMILARITY.  
 FT DISULFID 235 236 REACTIVE BOND (BY SIMILARITY).  
 FT CARBOHYD 141 141 BY SIMILARITY.  
 FT CARBOHYD 254 254 (POTENTIAL).  
 FT CARBOHYD 264 264 (POTENTIAL).  
 FT CARBOHYD 282 282 (POTENTIAL).  
 FT VARSPLIC 218 253 TKEENGGNAADYQGFESVTHLYPFVRIG (IN  
 FT VARSPLIC 254 306 ISOFORM BETA).  
 FT CONFFLICT 68 68 MISSING (IN ISOFORM BETA).  
 SQ SEQUENCE 306 AA; 34987 MW; D3EA329754B6A359 CRC64;



FT	CONFLICT	209	209	T -> G (IN REF. 4).	CC	the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
FT	CONFLICT	217	217	A -> D (IN REF. 4).	CC	
FT	CONFLICT	268	268	G -> I (IN REF. 2 AND 3).	CC	
FT	CONFLICT	268	274	E -> Q (IN REF. 2 AND 3).	CC	
FT	CONFLICT	274	298	SY -> AF (IN REF. 2 AND 3).	CC	
FT	CONFLICT	298	330	E -> Q (IN REF. 2 AND 3).	CC	
FT	CONFLICT	330	346	E -> R (IN REF. 2 AND 3).	CC	
FT	CONFLICT	346	352	MW; ED31CCACA02E70B19 CRC64;	DR	EMBL: D31B13; BAA06600_1; -
SEQUENCE		AA;		HSSP; P02760; 1B1K.	DR	InterPro; IPR002223; Kunitz_BPTI.
				InterPro; IPR002345; Lipocalin.	DR	InterPro; IPR002345; Lipocalin.
				InterPro; IPR000566; Lipocalin_cytFABP.	DR	InterPro; IPR000566; Lipocalin_cytFABP.
				Pfam; PF00014; Kunitz_BPTI_2.	DR	Pfam; PF00014; Kunitz_BPTI_2.
				Pfam; PF00061; Lipocalin_1.	DR	Pfam; PF00061; Lipocalin_1.
				PRINTS; PRO0759; BASICPTASE.	DR	PRINTS; PRO0759; BASICPTASE.
				PRINTS; PRO0179; LIPOCALIN.	DR	PRINTS; PRO0179; LIPOCALIN.
				SMART; SM00131; KU_2.	DR	SMART; SM00131; KU_2.
				PROSITE; PS00280; BPTI_KUNITZ_1; 2.	DR	PROSITE; PS00280; BPTI_KUNITZ_1; 2.
				PROSITE; PS550275; BPTI_KUNITZ_2; 2.	DR	PROSITE; PS550275; BPTI_KUNITZ_2; 2.
				KW Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat; Lipocalin.	DR	KW Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat; Lipocalin.
				KW Lipocalin.	DR	KW Lipocalin.
Query Match		26.3%	Score 249.5; DB 1; Length 352;	FT SIGNAL	1	19
Best Local Similarity		32.4%	Pred. No. 1; 3e-16;	FT CHAIN	20	202
Matches		48;	Conservative	FT CHAIN	205	346
			Mismatches 45;	FT CHAIN	205	346
			Gaps 1;	FT CHAIN	205	346
Qy	9	DFCLVSKVYGRGRSARVGRASPRWVNVNTDGSQCLFLVYGGDGNSNNVNLTKEECLKKCATVTEA 68	BY SIMILARITY.			
Do	229	DSQDLYSQQGPCLFLKFLYFNGTSMACETFYGGCNGNGNIFLSKECLOTCRTV-- 284	ALPHA-1 MICROGLOBULIN.			
Qy	69	TGDLATSRNAADSSVPSAPRQDSEDHSSDMNEYEEYCTANAVTGPGRASPRWYFDVER 128	INTER-ALPHA-TRYPSIN INHIBITOR LIGHT CHAIN.			
Do	285	-- 310 GRCVRFSYGGCKGNGNKFYSKECKEYK 337	BPTI_KUNITZ INHIBITOR 1.			
Qy	129	NSCNNFIYGGCGNKNYSRSEACMLRC 156	BPTI_KUNITZ INHIBITOR 2.			
Do	310	GRCVRFSYGGCKGNGNKFYSKECKEYK 337	CHROMOPHORE (BY SIMILARITY).			
Do	285	-- 309 -EACNLPIVQGPGRCSYIQLWAFDAVK 309	DISULFID	52	52	
RESULT 7			DISULFID	90	187	
AMBP_MERUN		STANDARD; PRT; 346 AA.	DISULFID	230	280	
ID	AMBP_MERUN	STANDARD; PRT; 346 AA.	DISULFID	239	263	
AC	062577; 062576;		DISULFID	239	263	
DT	01-NOV-1997 (Rel. 35, Created)		DISULFID	255	276	
DT	01-NOV-1997 (Rel. 35, Last sequence update)		DISULFID	286	336	
DT	16-OCT-2001 (Rel. 40, Last annotation update)		DISULFID	295	319	
DE	AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30)].		DISULFID	311	332	
GN	AMBPOFITL.		DISULFID	311	332	
OS	Meriones unguiculatus (Mongolian jird).		DISULFID	314	334	
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae; Meriones.		DISULFID	314	334	
OC	NCBI_TaxID=10047;		DISULFID	314	334	
RN	[1]		DISULFID	314	334	
RP	SEQUENCE FROM N. A.		DISULFID	314	334	
RC	TISSUE-Liver;		DISULFID	314	334	
RX	MEDLINE:95110820; PubMed=7529051;		DISULFID	314	334	
RA	Ide H., Itoh H., Nawa Y.;		DISULFID	314	334	
RA	Mongolian gerbil and Syrian golden hamster in comparison with man and other species";		DISULFID	314	334	
RL	Blophys, Acta 1209:286-292 (1994).		DISULFID	314	334	
CC	- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA AND ALBUMIN BY SIMILARITY.		DISULFID	314	334	
CC	- FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSSOMAL GRANULOCYTIC ELASTASE (BY SIMILARITY).		DISULFID	314	334	
CC	CC - SUBUNIT: I-ALPHA-1 plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, bikunin. Inter-alpha-inhibitor (I-ALPHA-1) is composed of H1, H2 and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and bikunin, and pre-alpha-inhibitor (P-ALPHA-1) of H3 and bikunin (BY SIMILARITY).		DISULFID	314	334	
CC	- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO SEPARATELY FUNCTIONING PROTEINS.		DISULFID	314	334	
CC	- PTM: Alpha-1-microglobulin contains a covalently linked brown-yellow chromophore (BY similarity).		DISULFID	314	334	
CC	- SIMILARITY: IN THE N TERMINAL SECTION; BELONGS TO THE LIPOCALIN FAMILY.		DISULFID	314	334	
CC	- SIMILARITY: CONTAINS 2 BPTI_KUNITZ INHIBITOR DOMAINS.		DISULFID	314	334	
CC	CC - This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -		DISULFID	314	334	
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OX	RN	[1]	SEQUENCE FROM N.A.
	RP		SEQUENCE -SPRAGUE-DAWLEY; TISSUE=Liver;
	RC		
	RX		MEDLINE=92348361; PubMed=1639167;
	RA		ENJOJI K.-I.; Enri M.; Mukai T.; Kato H.;
	RA		"cDNA cloning and expression of rat tissue factor pathway inhibitor (TFPI)."
	RT		J. Biochem. 111:681-687(1992).
	RL		-1- FUNCTION: INHIBITS FACTOR X (Xa) DIRECTLY AND, IN A Xa-DEPENDENT WAY, INHIBITS VII (A) / TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING A QUATERNARY Xa/TF/TFI(VIIa)/TF COMPLEX. IT POSSESSES AN ANTIHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH LIPOPROTEINS IN PLASMA.
	CC		-1- TISSUE SPECIFICITY: MOST ABUNDANT IN HEART, LUNG, KIDNEY, AND AORTIC ENDOTHELIAL CELLS.
	CC		-1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
	CC		-1- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
	CC		
	CC		This SWISS-PROT entry is copyright. It is produced through collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
	CC		
	CC		-----
	CC		EMBL: D10926; BAA01724..1. -.
	DR		PIR: JX0213; TIRPTK.
	DR		HSSP: P1046; ITFX.
	DR		Inter-Pro: IPR02223; Kunitz_BPTI.
	DR		Pfam: PF00014; Kunitz_BPTI; 3.
	DR		PRINS: PR00750; BASICPROFASE.
	DR		SM00131; KU; 3.
	DR		PROSTATE; PS00280; BPTI_KUNITZ_1; 3.
	DR		PROSTATE; PS50229; BPTI_KUNITZ_2; 3.
	DR		Protease inhibitor; Glycoprotein; Repeat; Blood coagulation; Signal.
	FT	1	28
	FT	29	302
	FT	53	103
	FT	124	174
	FT	222	272
	FT	53	103
	FT	62	86
	FT	78	99
	FT	63	64
	FT	124	174
	FT	133	157
	FT	149	170
	FT	134	135
	FT	222	272
	FT	231	255
	FT	247	268
	FT	232	233
	FT	144	144
	FT	251	251
	FT	261	261
	FT	302	AA: MW: 34554
	FT		F9AE8213024A59F CRC64;
	FT		
	FT		-----
	FT		Query Match 26 0%; Score 246.5%; DB: 1; Length 302;
	FT		Best Local Similarity 34.0%; Pred. No. 2.2e-16;
	FT		Matches 54; Conservative 21; Mismatches 65; Indels 19; Gaps 3;
	FT		
	FT		-----
	FT		Qy 9 DFLCVSKVYCRASPRMWWYNTDGSQCLFYGGCGDGSNNYLTKEEKKKA-TVYEN 67
	Db		122 DFCFLDEDPGICRFEMTRFYNNOSKQCEQFYGGCLGNNPFTELBRCNTCDPYNEV 181
	FT		
	FT		-----
	FT		Qy 68 ATGDLATSR- NAADSSVSPARRDSDHSSDMNYYEFTANAVTGVGCR 117

Db	182	QKGDDYVNTQITVTDRTTVNNTVIPQATKAPSQWDYDGPS-----WCLEPADSGLCKA	233
Qy	118	SEPRFWFDEVRNSCNFPIYGCGRKNNFSRREACMRLRC	156
	118	:  :  :  :  :  :  :  :  :  :  :  :  :  :  :	:  :  :  :  :  :  :  :  :  :  :  :  :  :
Db	234	SEKRFYVNPAGKCRQFNFTGCGNNNNFTIKQDCNRAC	272
	234	:  :  :  :  :  :  :  :  :  :  :  :  :  :  :	:  :  :  :  :  :  :  :  :  :  :  :  :  :
RESULT 9			
	IATR_SHEEP	STANDARD;	PRT;
	ID	IATR_SHEEP	123 AA.
	AC	P13371;	
	DT	01-JAN-1990 (Rel. 13, Created)	
	DT	01-JAN-1990 (Rel. 13, Last sequence update)	
	DT	16-OCT-2001 (Rel. 40, Last annotation update)	
	DE	Inter-alpha-trypsin inhibitor (ITI) (GIK-14) (Inhibitory fragment of ITI) (Fragment).	
	DE	Ovis aries (Sheep), and	
	OS	Capra hircus (Goat).	
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae; Caprinae; Ovis.	
	OC	NCBI_TaxID=9940, 9925;	
	OX	[1]	
	RN	RP	
	RC	SEQUENCE.	
	RC	SPECIES=C_hircus;	
	RC	MEDLINE=91010540; PubMed=2481505;	
	RA	Rasp G., Hochstrasser K., Gerl C., Wachter E ;	
	RT	Primary structure of a protease inhibitor released from goat serum inter-alpha-trypsin inhibitor.	
	RT	Blochim. Biophys. Acta 999:3335-337 (1989).	
	RL	-1- FUNCTION: THIS INHIBITORY FRAGMENT, RELEASED FROM NATIVE ITI AFTER LIMITED PROTEOLYSIS WITH TRYPSIN, CONTAINS TWO HOMOLOGOUS DOMAINS WHEREAS THE SECOND DOMAIN IS A STRONG INHIBITOR OF TRYPSIN, THE FIRST DOMAIN INTERACTS WEAKLY WITH PAN-GRANULOCYTIC ELASTASE AND NOT AT ALL WITH PANCREATIC ELASTASE.	
	CC	-1- MISCELLANEOUS: THE AMINO ACID AT POSITION P2' (17) APPEARS TO DETERMINE THE SPECIFICITY OF THE INHIBITION OF DOMAIN I. INHIBITORS WITH METHIONINE IN THIS POSITION INTERACT WEAKLY WITH CHYMOTRYPSIN AND ELASTASE; THOSE WITH LEUCINE INTERACT STRONGLY.	
	CC	-1- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.	
	CC	PTR; A29652; A29652.	
	DR	HSSP; P02760; 1B1K.	
	DR	InterPro; IPR002223; Kunitz_BPTI.	
	DR	Pram; PF00014; Kunitz_BPTI; 2.	
	DR	SMART; SMM00131; KU; 2.	
	DR	PROSITE; PS00280; BPTI_KUNITZ_1; 2.	
	DR	PROSITE; PS00279; BPTI_KUNITZ_2; 2.	
	KW	Plasma Glycoprotein; Serine protease inhibitor; Repeat.	
	FT	NON_TER 1 . 1	
	FT	DOMAIN 5 . 55	
	FT	DOMAIN 61 111	
	FT	DISULFID 55 55	
	FT	DISULFID 14 38	
	FT	DISULFID 30 51	
	FT	DISULFID 61 111	
	FT	DISULFID 70 94	
	FT	DISULFID 86 107	
	FT	ACT_SITE 15 16	
	FT	BPTI/KUNITZ INHIBITOR 1.	
	FT	BPTI/KUNITZ INHIBITOR 2.	
	FT	DISULFID 55 55	
	FT	DISULFID 14 38	
	FT	DISULFID 30 51	
	FT	DISULFID 61 111	
	FT	DISULFID 70 94	
	FT	DISULFID 86 107	
	FT	ACT_SITE 15 16	
	FT	INHIBITORY SITE (P1) (CHYMOTRYPSIN, ELASTASE).	
	FT	INHIBITORY SITE (P1) (TRYPSIN).	
	FT	N LINKED (GLCNAC. . ).	
	FT	CARBOHYD 24 24	
	FT	NON_TER 123 123	
	SEQUENCE	123 AA; 13686 MN; 295038173F22D2D1 CRC64;	
SQ		25.8%; Score 244.5; DB 1; Length 123;	
		Query Match	

Best Local Similarity	31.8%	Pred. No.	1.2e-16	Matches	47;	Mismatches	47;	Indels	39;	Gaps	1;	
Matches	47;	Conservative	15;									"Human protein HC displays variability in its carboxyl-terminal amino acid sequence";
QY	9	DFCLVSKVYGRCRASMRMWWYNTDGSCQLFYGGCGNSNNMLTRECLKKCATVENA	68									RT
QY	3	DSQGLGYSQGPCLGMFARYNGTSMACETFYGGCMNGNNFSEKLCQTCRTV	58									RT
QY	69	TGDLATSRNAADSSVSPSAPRQDSEHDSSDMFNYEEYCTANAVTGPGRASPRWYFDEVER	128									RT
DB	59	-----QACNLPLIVRGPCRAGIELWAFDAVK	83									RT
DB	129	NSCNNFIYGGCRGNKNSYRSEBACMLRC	156									RT
DB	84	GKCVRFIYGGCNGNGNQFSQKECKEYC	111									RT
RESULT 1.0												
AMB_P_HUMAN	ID	AMB_P_HUMAN	STANDARD;	PRT;	352	AA.						RT
AC	AC	P02759;	PubMed=80	01;	21-JUL-1986	(Rel. 01; Created)						RT
DT	DT	13-AUG-1987	(Rel. 05; Last sequence update)									RT
DT	DT	16-AUG-2001	(Rel. 40; Last annotation update)									RT
DE	DE	AMB_P protein precursor [Contains: Alpha-1-microglobulin (Protein HC) (Complex-forming glycoprotein heterogeneous in charge); Inter-alpha-trypsin inhibitor light chain (ITI-Lc) (Bikunin) (HI-30);]										DE
GN	GN	AMB_P OR ITIL OR HC_P.										DE
OS	OS	Homo sapiens (Human);										OS
OC	OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										OC
OC	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.										OC
OX	OX	NCBI_TAXID=9606;										OX
RN	RN											RN
RP	RP	SEQUENCE FROM N.A.										RP
RX	RX	MEDLINE=91214554; PubMed=1708673;										RX
RA	RA	Verl H., Gebhard W.;										RA
RT	RT	"Structure of the human alpha 1-microglobulin-bikunin gene.";										RT
RL	RL	Biol. Chem. Hoppe-Seyler 371:1185-1196(1990).										RL
RN	RN											RN
RP	RP	SEQUENCE FROM N.A.										RP
RC	RC	TISSUE=liver										RC
RX	RX	MEDLINE=87040757; PubMed=2430261;										RX
RA	RA	Kaumeyer J.F., Polazzi J.O., Kotick M.P.;										RA
RT	RT	"The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-trypsin inhibitor also encodes alpha-1-microglobulin (protein HC).";										RT
RT	RT	Nucleic Acids Res. 14:7839-7850(1986).										RT
RN	RN	[13]										RN
RP	RP	SEQUENCE FROM N.A.										RP
RC	RC	TISSUE=liver										RC
RX	RX	MEDLINE=90336621; PubMed=1696200;										RX
RA	RA	Diarra-Mehrpour M., Bourguignon J., Sesboue R., Salier J.P.;										RA
RA	RA	Leveillard T., Martin J.P., Kotick M.P.;										RA
RT	RT	"Structural analysis of the human inter-alpha-trypsin inhibitor light-chain gene";										RT
RT	RT	Nucleic Acids Res. 19:131-139(1990).										RT
RN	RN	[14]										RN
RP	RP	SEQUENCE OF 1-220 FROM N.A.										RP
RX	RX	MEDLINE=86312901; PubMed=2428011;										RX
RA	RA	Traboni C., Cortese R.;										RA
RT	RT	"Sequence of a full length cDNA coding for human protein HC (alpha 1-microglobulin).";										RT
RT	RT	Nucleic Acids Res. 14:6340-6340(1986).										RT
RN	RN	[15]										RN
RP	RP	SEQUENCE OF 20-202 (INDIVIDUAL WITH TUBULAR PROTEINURIA).										RP
RX	RX	MEDLINE=84126849; PubMed=6198962;										RX
RA	RA	Lopez C., Grubb A.O., Mendez E.;										RA
RT	RT	"The complete amino acid sequence of human complex-forming glycoprotein heterogeneous in charge (protein HC) from one individual.";										RT
RA	RA	Arch. Biochem. Biophys. 228:544-554(1984).										RA
RP	RP	SEQUENCE OF 20-198 (VARIANT).										RP
RA	RA	Pizzo S.V., Pizzo S.V.;										RA
RA	RA	"Chondroitin 4-sulfate covalently cross-links the chains of the human										RA

"Human protein HC displays variability in its carboxyl-terminal amino acid sequence";

FEBS Lett. 144:349-353(1982).

SEQUENCE OF 20-198 (PATIENTS WITH TUBULAR PROTEINURIA).

MEDLINE=81180438; PubMed=6164372;

Takagi T., Takagi K., Kawai T.;

"Complete amino acid sequence of human alpha 1-microglobulin.";

Biochem. Biophys. Res. Commun. 98:997-1001(1981).

SEQUENCE OF 206-350.

MEDLINE=85225968; PubMed=2408638;

Reisinger P., Hochstrasser K., Albrecht G.J., Lempart K., Salier J.P.;

"Human inter-alpha-trypsin inhibitor; localization of the Kunitz-type domains in the N-terminal part of the molecule and their release by a trypsin-like protease.";

Biochim. Hoppe-Seyler 366:479-483(1985).

SEQUENCE OF 206-350.

MEDLINE=82074265; PubMed=6171477;

Hochstrasser K., Schoenberger O.J., Rossmanith I., Wachter E.;

"Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor. V. Attachments of carbohydrates in the human urinary trypsin inhibitor isolated by affinity chromatography.";

Biochim. Hoppe-Seyler's Z. Physiol. Chem. 362:1357-1362(1981).

SEQUENCE OF 206-350.

MEDLINE=85225940; PubMed=3890890;

Morii M., Travis J.;

"The reactive site of human inter-alpha-trypsin inhibitor is in the amino-terminal half of the protein.";

Biochim. Hoppe-Seyler 366:19-21(1985).

SEQUENCE OF 206-350.

MEDLINE=90306345; PubMed=6194784;

Escribano J., Lopez-Otin C., Hjerpe A., Grubb A.O., Mendez E.;

"Location and characterization of the three carbohydrate prosthetic groups of human protein HC.";

FEBS Lett. 266:167-170(1990).

SEQUENCE OF 206-219, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.

TISSUE=Plasma;

MEDLINE=91140714; PubMed=1714898;

Escrivano J., Grubb A.O., Calero M., Mendez E.;

"The protein HC chromophore is linked to the cysteine residue at position 34 of the polypeptide chain by a reduction-resistant bond and causes the charge heterogeneity of protein HC.";

J. Biol. Chem. 266:15758-15763(1991).

SEQUENCE OF 206-219, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.

MEDLINE=94229087; PubMed=7513643;

Morelle W., Capon C., Baldyuck M., Sautiere P., Kouach M., Michalski C., Fournet B., Mizon J.;

"Chondroitin sulphate covalently cross-links the three polypeptide chains of inter-alpha-trypsin inhibitor";

Eur. J. Biochem. 221:1881-1888(1994).

SEQUENCE OF 206-223, AND CROSS-LINK SITE TO HC2.

MEDLINE=93332026; PubMed=7682553;

Englund J.J., Salvesen G., Thoegersen I.B., Valnickova Z.;

"Presence of the protein-glycosaminoglycan-protein covalent cross-link in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain 2/bikinin.";

J. Biol. Chem. 266:15758-15763(1991).

SEQUENCE OF 206-223, AND CROSS-LINK SITE TO HC3.

MEDLINE=91093267; PubMed=1898736;

Englund J.J., Salvesen G., Hefta S.A., Thoegersen I.B.;

"Chondroitin 4-sulfate covalently cross-links the chains of the human

blood protein pre-alpha-inhibitor.";

RL J. Biol. Chem. 266:747-751(1991).  
RN [16]

RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 230-339.  
MEDLINE=98227321; PUBMED=9566199;

RA Xu Y.; Carr P.D.; Guss J.M.; Ollis D.L.;  
RT "The crystal structure of bikunin from the inter-alpha-inhibitor  
complex: a serine protease inhibitor with two Kunitz domains."  
J. Mol. Biol. 276:955-966(1998).

-I- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL  
FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT  
APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA  
AND ALBUMIN.

CC FUNCTION: INVER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND  
URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC  
ELASTASE. ADDITIONAL PROTEOLYTIC PROCESSING IN THE KIDNEY AND/OR  
URINE CAN PRODUCE FURTHER AMINO- AND CARBOXYL-END MODIFICATIONS  
IN ITS SEQUENCE.

CC SUBUNIT: I-ALPHA-1 plasma protease inhibitors are assembled from  
one or two heavy chains (H1, H2 or H3) and one light chain,  
bikunin. Inter-alpha-inhibitor (I-ALPHA-1) is composed of H1, H2  
and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and  
bikunin, and pre-alpha inhibitor (P-ALPHA-1) of H3 and bikunin (By  
similarity).

-I- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO  
SEPARATELY FUNCTIONING PROTEINS.

-I- PTM: Alpha-1-microglobulin contains a covalently linked brown-  
CC yellow chromophore.

CC PTM: ADDITION OF GLYCOSAMINOGLYCAN CHONDROITIN SULFATE, ALLOWS  
CROSS-LINKING BETWEEN THE DIFFERENT COMPONENTS.

-I- MISCELLANEOUS: IN VITRO, THE FIRST TWELVE RESIDUES OF THE AMINO  
END OF THE INHIBITOR APPEAR TO HAVE A REACTIVE SITE CAPABLE OF  
INHIBITING THE ACTIVITY OF A NUMBER OF ENYMES. ITS IN VIVO  
FUNCTION IS NOT KNOWN.

CC SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN  
FAMILY.

CC SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.

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or send an email to license@isb-sib.ch).

CC EMBL; X54816; CAA38585.1; -;  
DR EMBL; X54817; CAA38585.1; -;  
DR EMBL; X54818; CAA38585.1; -;  
DR EMBL; X04225; CAA27803.1; -;  
DR EMBL; M88249; AA59196.1; -;  
DR EMBL; M88165; AA59196.1; JOINED.  
DR EMBL; M88243; AA59196.1; JOINED.  
DR EMBL; M88244; AA59196.1; JOINED.  
DR EMBL; M88246; AA59196.1; JOINED.  
DR EMBL; M88247; AA59196.1; JOINED.  
DR EMBL; X04494; CAA28182.1; -;  
DR PIR; X54817; HCRU; -;  
DR PIR; A03217; HCRU; -;  
DR PIR; A25303; A25303;  
DR PIR; S13433; S13433;  
DR PIR; S10717; S10717;  
DR PDB; 1EIK; 16-MAR-99;  
DR GLYCOSITES; P02760; -;  
DR SWISS-PPD PAGE; P02760; -;  
DR SIENA-2DPAGE; P02760;  
DR PDB; 176870; -;  
DR InterPro; IPR002223; Kunitz\_BPTI.  
DR InterPro; IPR003345; Lipocalin.  
DR Pfam; PF00014; Kunitz\_BPTI; 2.  
DR Pfam; PF00061; Lipocalin; 1.

Query Match 25.8%; Score 244.5; DB 1; Length 352;  
Best Local Similarity 32.4%; Pred. No. 4e-16;  
Matches 48; Conservative 14; Mismatches 47; Indels 39; Gaps 1;

Qy 9 DECLVSKVVGCRASHPRWWNVTGDSQLEVYGGDGSNNVLYTKECLKKCATVTEA 68  
Db 229 DSCQLGYSAGCMGMSRTSYFNGTSMACTEQYGGMGNINFVTEKCLQTCRVAA-- 286

Qy 69 TGDLATSRNAADSSVPSAPRQDSEDSHSDMFNEYCTANAVTGPGRASPRNFVDR 128  
Db 287 -----CLNLPIVRGFCRAFIQLWADAVK 309

Qy 129 NSCNNFIYGGCRGNKNSYRSEACMLRC 156  
Db 310 GRCVLPYGGCQGNGKRYSKKECREYC 337

RESULT 11  
TPPI\_RABBIT  
ID TPPI\_RABBIT STANDARD;  
AC P19761; Q28828;  
DR 01-AUG-1991 (Rel. 17, Created)  
DR 01-AUG-1992 (Rel. 23, Last sequence update)  
DR 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-  
DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)  
DE (EPI).  
GN TFPI.  
OS Oryctolagus cuniculus (Rabbit).  
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.  
OX NCBI\_TaxID=986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Liver;  
RX MEDLINE=91057146; PubMed=2136251;  
RA Wesselschmidt R.L.; Girard T.J.; Broze G.J. Jr.;  
RT "CDNA sequence of rabbit lipoprotein-associated coagulation  
inhibitor."  
RN [2]  
RN REVISIONS TO 72; 211 AND 218.  
RC TISSUE-Liver;  
RX MEDLINE=92335027; PubMed=1630940;  
RA Warn-Cramer B.J.; Broze G.J. Jr.; Komives E.A.;  
RT "CDNA sequence of rabbit tissue factor pathway inhibitor."  
RN Nucleic Acids Res. 18:6440-6440(1999).  
RN SEQUENCE FROM N.A.  
RC TISSUE-Lung;  
RX MEDLINE=93276427; PubMed=9503123;  
RA Belaaouaj A.; Kuppusamy M.N.; Birktoft J.J.; Bajaj S.P.;  
RT "Revised cDNA sequence of rabbit tissue factor pathway inhibitor."  
RL Thromb. Res. 69:547-553 (1993).  
CC -I- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT  
WAY, INHIBITS VII(A) TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING  
A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN  
CC ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH  
CC LIPOPROTEINS IN PLASMA.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.  
CC -I- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.  
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or send an email to license@isb-sib.ch).

CC -I- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.  
CC -I- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.  
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or send an email to license@isb-sib.ch).

DR X54708; CAA38586.1; -;  
DR Pfam; PF00014; Kunitz\_BPTI; 2.  
DR Pfam; PF00061; Lipocalin; 1.

DR	PIR; S12143; S12143.
DR	HSSP; P10646; 1TFX.
DR	InterPro; IPR002223; Kunitz_BPTI.
DR	Pfam; PF00014; Kunitz_BPTI; 3.
PRINTS	SMART; SMR0131; KU; 3.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 3.
DR	Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation; Signal.
SIGNAL	1 24
CHAIN	25 300
FT	FT TISSUE FACTOR PATHWAY INHIBITOR.
FT	FT BPTI/KUNITZ INHIBITOR 1
FT	FT (VII(A) TISSUE FACTOR BINDING SITE).
FT	FT BPTI/KUNITZ INHIBITOR 2
FT	FT (FACTOR XA) BINDING SITE.
FT	FT BPTI/KUNITZ INHIBITOR 3
FT	FT (BY SIMILARITY).
FT	FT BY SIMILARITY.
FT	FT BY SIMILARITY.
FT	FT BY SIMILARITY.
FT	FT REACTIVE BOND (BY SIMILARITY).
FT	FT BY SIMILARITY.
FT	FT REACTIVE BOND (BY SIMILARITY).
FT	FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT MISSING (IN REF. 3).
FT	FT PKSI. > FNLS (IN REF. 3).
FT	FT
SEQUENCE	300 AA; 34435 MW; A08DE3537708CA6 CRC64;
Query Match	25.7% Score 244; DB 1; Length 300;
Best Local Similarity	30.0% Pred. No. 3.7e-16;
Matches	48; Conservative 23; Mismatches 61; Indels 28; Gaps
Qy	4 ERSIHDFELVSKVGRCRASMPMRWVNTDGSQFLTVGGCDONSNNLTIKECLKKAT 63
Db	43 QKPTHSFCAMKVDGPGCRAYIKREFFENNLTHQOEEFIYGGCEENENRFESLECKERCAR 10
Qy	64 VTNENATGDLATRNSAADDVSSPAAPRQDSEDHSSDMFNEYCTANAVTGPGRASFRWY 12
Db	103 DPKMTKTLTQFGKPD-----PFCLEEDPGICRGYITRYF 13
Qy	124 FDVERNSCNNFYIYGGCRGNKNSYRSEEACMLRCFRQQENP 163
Db	139 YNNOSKQCREFYYGGCLGNLNFFESLECKNTL---ENP 174
RESULT 12	
AMB_PIG	AMB_PIG STANDARD; PRT; 337 AA.
AC	P04366; P34954; STANDARD; PRT; 337 AA.
DT	20-MAR-1987 (Rel. 04, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	AMB_P protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha trypsin inhibitor light chain (I-1-LC) (Bikunin) (HI-30) (EI-14)] (Fragment)
DE	AMB_P OR I-1-LC.
GN	Sus scrofa (Pig).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID	9823;
[1]	SEQUENCE FROM N_A.
RN	RP
MEMLINE#005395; PubMed:1666914;	
Gebhard W.; Schreitmüller T.; Vetr H.; Wachter E.; Hochstrasser K.;	

"Complementary DNA and deduced amino acid sequences of procine alpha 1-microglobulin and bikunin.";  
RT RL FEBS Lett. 269:32-36 (1990).  
RN [2]  
SEQUENCE OF 2-337 FROM N.A.  
RN RP TISSUE-Liver;  
RN RX MEDLINE=91113729; PubMed=1703444;  
RA Tavakkol A;  
RT "Molecular cloning of porcine alpha 1-microglobulin/Hi-30 reveals developmental and tissue-specific expression of two variant messenger ribonucleic acids.";  
RT Bioclin. Biophys. Acta 1088:47-56(1991).  
RN [3]  
SEQUENCE OF 212-334.  
RX MEDLINE=85225967; PubMed=2408637;  
RA Hochstrasser K.; Wachter B.; Albrecht G.J.; Reisinger P.;  
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the trypsin-released inhibitors from horse and pig inter-alpha-trypsin inhibitors.";  
RT Biol. Chem. Hoppe-Seyler 366:473-478(1985).  
CC CC FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA AND ALBUMIN.  
CC CC -1- FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND URINE, INHIBITS TRYPSIN, PLASMIN, AND LYPOSOMAL GRANULOCYTIC ELASTASE.  
CC CC -1- SUBUNIT: I-ALPHA-1 plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, CC CC bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2 and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (BY similarity).  
CC CC -1- PRECURSOR: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO SEPARATELY FUNCTIONING PROTEINS.  
CC CC -1- PTM: Alpha-1-microglobulin contains a covalently linked brown-yellow chromophore.  
CC CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE LIPOCALIN FAMILY.  
CC CC -1- SIMILARITY: CONTAINS 2 BPT1/KUNITZ INHIBITOR DOMAINS.  
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CC DR EMBL; X53685; CAA37755.1;  
DR EMBL; X52087; CAA36306.1;  
DR PIR; A01208; TIGB1.  
DR PIR; S11066; S11066.  
DR HSSP; P02760; IBK.  
DR InterPro; IPR002223; Kunitz\_BPT1.  
DR IPR000566; Lipocalin\_cytFABP.  
DR Pfam; PF00014; Kunitz\_BPT1; 2.  
DR Pfam; PE00061; Lipocalin; 1.  
DR SMART; SM00131; RU; 2.  
DR PROSITE; PS000280; BPT1\_KUNITZ\_1; 2.  
DR PROSITE; PS500279; BPT1\_KUNITZ\_2; 2.  
DR PROSITE; PS00213; LIPOCALIN; 1.  
DR Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat; Lipocalin.  
KW KW BY SIMILARITY.  
FT FT ALPHA-1-MICROGLOBULIN.  
FT FT INTER-ALPHA-TRYPSIN INHIBITOR 1.  
FT FT CHAIN.  
FT FT BPT1/KUNITZ INHIBITOR 1.  
FT FT CHROMOPHORE (BY SIMILARITY).  
FT FT CHROMOPHORE (BY SIMILARITY).  
FT FT DOMAIN 216 266  
FT FT DOMAIN 272 322  
FT FT BINDING 38 38



RA Kido H., Yokogoshi Y., Karunuma N.;  
 RT "Kunitz type protease inhibitor found in rat mast cells. Purification,  
 properties, and amino acid sequence.";  
 J. Biol. Chem. 263:18104-18107(1988).;

RA [4]

RP PROCESSING;

RX MEDLINE:94148892; PubMed=7508921;

RX "Mast cell protease inhibitor, trypstatin, is a fragment of  
 inter-alpha-trypsin inhibitor light chain.";

RX J. Biol. Chem. 269:3818-3820(1994).

CC -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL  
 FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT  
 APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA  
 AND ALBUMIN (BY SIMILARITY).

CC -!- FUNCTION: INVER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND  
 URINE, INHIBITS TRYPSIN, PLASMIN, AND LYMPHOCYTIC  
 ELASTASE (BY SIMILARITY).

CC -!- FUNCTION: Trypsatin is a trypsin inhibitor. It inhibits blood  
 coagulation factor Xa and trypsin about 100-fold more rapidly  
 than porcine pancreatic trypsin and chymase. It is a monomer but  
 is also found in mast cells as a complex with trypase.

CC -!- SUBCELLULAR LOCATION: I-ALPHA-1 plasma protease inhibitors are assembled from  
 one or two heavy chains (H1, H2 or H3) and one light chain,  
 bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2  
 and bikunin. Inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and  
 bikunin, and pre-alpha-inhibitor (P-ALPHA-T) of H3 and bikunin (BY  
 SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Trypsatin is present in mast cell granules.

CC -!- PRM: The precursor is proteolytically processed into separately  
 bikunin, Inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and  
 bikunin, and pre-alpha-inhibitor (P-ALPHA-T) of H3 and bikunin (BY  
 SIMILARITY).

CC -!- PRM: Heavy chains are interlinked with bikunin via a chondroitin  
 sulphate bridge to the their C-terminal aspartate (BY  
 SIMILARITY).

CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN  
 FAMILY.

CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.

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 or send an email to license@isb-sib.ch).

CC DR EMBL; J02600; AAA41598; 1; -;

CC DR PRINTS; PR00759; BASICPTASE.

CC DR PRINTS; PR00179; LIPOCALIN.

CC DR InterPro; IPR002223; Kunitz\_BPTI.

CC DR InterPro; IPR002345; Lipocalin.

CC DR Pfam; FE00014; Kunitz\_BPTI; 2.

CC DR Pfam; FE00061; Lipocalin; 1.

CC DR SMART; SM00131; KU; 2.

CC DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.

CC DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 2.

CC DR PROSITE; PS00113; LIPOCALIN; 1.

CC KW Lipocalin.

CC SIGNAL 1 19 BY SIMILARITY.

CC FT CHAIN 20 202 ALPHA-1-MICROGLOBULIN.  
 INTER-ALPHA-TRYPSIN INHIBITOR LIGHT CHAIN.

CC FT CHAIN 205 349 TRYPSATIN.

CC FT DOMAIN 230 280 BPTI/KUNITZ INHIBITOR 1.

CC FT DOMAIN 286 336 BPTI/KUNITZ INHIBITOR 2.

CC FT BINDING 52 52 CHROMOPHORE (BY SIMILARITY).

RA Kido H., Yokogoshi Y., Karunuma N.;  
 RT "Kunitz type protease inhibitor found in rat mast cells. Purification,  
 properties, and amino acid sequence.";  
 J. Biol. Chem. 263:18104-18107(1988).;

RA [4]

RP PROCESSING;

RX MEDLINE:94148892; PubMed=7508921;

RX "Mast cell protease inhibitor, trypstatin, is a fragment of  
 inter-alpha-trypsin inhibitor light chain.";

RX J. Biol. Chem. 269:3818-3820(1994).

CC -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL  
 FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT  
 APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA  
 AND ALBUMIN (BY SIMILARITY).

CC -!- FUNCTION: INVER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND  
 URINE, INHIBITS TRYPSIN, PLASMIN, AND LYMPHOCYTIC  
 ELASTASE (BY SIMILARITY).

CC -!- FUNCTION: Trypsatin is a trypsin inhibitor. It inhibits blood  
 coagulation factor Xa and trypsin about 100-fold more rapidly  
 than porcine pancreatic trypsin and chymase. It is a monomer but  
 is also found in mast cells as a complex with trypase.

CC -!- SUBCELLULAR LOCATION: Trypsatin is present in mast cell granules.

CC -!- PRM: The precursor is proteolytically processed into separately  
 bikunin, Inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and  
 bikunin, and pre-alpha-inhibitor (P-ALPHA-T) of H3 and bikunin (BY  
 SIMILARITY).

CC -!- PRM: Heavy chains are interlinked with bikunin via a chondroitin  
 sulphate bridge to the their C-terminal aspartate (BY  
 SIMILARITY).

CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN  
 FAMILY.

CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.

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 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 or send an email to license@isb-sib.ch).

RA Kido H., Yokogoshi Y., Karunuma N.;  
 RT "Kunitz type protease inhibitor found in rat mast cells. Purification,  
 properties, and amino acid sequence.";  
 J. Biol. Chem. 263:18104-18107(1988).;

RA [4]

RP PROCESSING;

RX MEDLINE:94148892; PubMed=7508921;

RX "Mast cell protease inhibitor, trypstatin, is a fragment of  
 inter-alpha-trypsin inhibitor light chain.";

RX J. Biol. Chem. 269:3818-3820(1994).

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 FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT  
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 FAMILY.

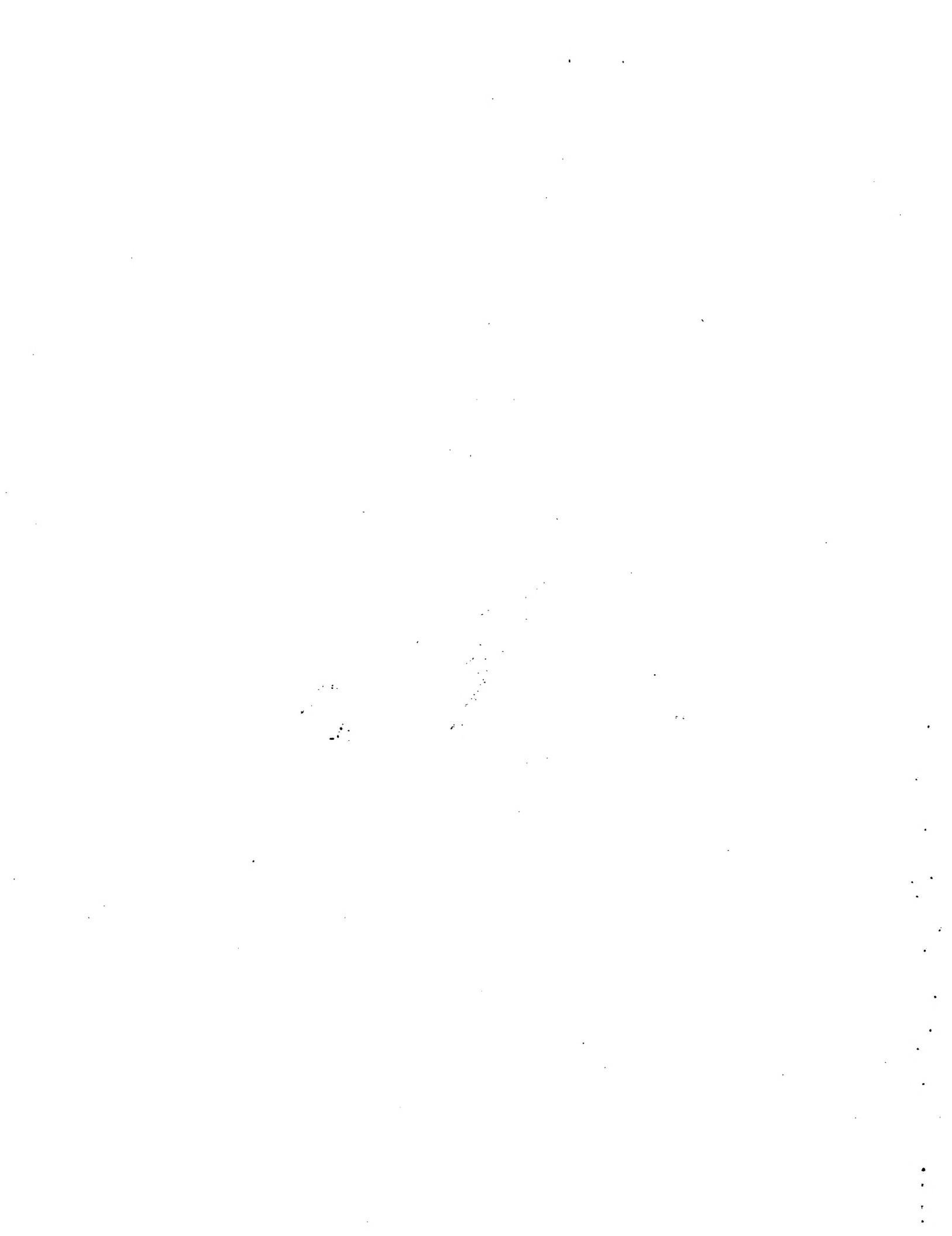
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.

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DR EMBL; S73337; AAB31955.1;  
 DR HSPP; P10646; ITPX.  
 DR InterPro; IPR00223; Kunitz\_BPTI.  
 DR Pfam; PF0014; Kunitz\_BPTI\_3.  
 DR PRINTS; PRO0759; BASICPTASE.  
 DR SMART; SM00131; KU; 3.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1;  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 3.  
 KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;  
 KW Signal  
 FT SIGNAL . 1 28 BY SIMILARITY.  
 FT CHAIN . 29 304 TISSUE FACTOR PATHWAY INHIBITOR.  
 FT DOMAIN . 54 104 BPTI/KUNITZ INHIBITOR 1  
 FT DOMAIN \ 125 175 (VII(A))TISSUE FACTOR BINDING SITE).  
 FT DOMAIN 217 267 BPTI/KUNITZ INHIBITOR 2  
 FT DISULFID 54 104 (FACTOR X(A)) BINDING SITE).  
 FT DISULFID 63 87 BPTI/KUNITZ INHIBITOR 3.  
 FT DISULFID 79 100 BY SIMILARITY.  
 FT ACT\_SITE 64 65 BY SIMILARITY.  
 FT DISULFID 125 175 REACTIVE BOND (BY SIMILARITY).  
 FT DISULFID 134 158 BY SIMILARITY.  
 FT DISULFID 150 171 BY SIMILARITY.  
 FT ACT\_SITE 135 136 REACTIVE BOND (BY SIMILARITY).  
 FT DISULFID 217 267 BY SIMILARITY.  
 FT DISULFID 226 250 BY SIMILARITY.  
 FT DISULFID 242 263 BY SIMILARITY.  
 FT ACT\_SITE 227 228 REACTIVE BOND (BY SIMILARITY).  
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 256 256 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 304 AA: 35085 MW: 56E13B3FF16282H0 CRC64;  
 QY Query Match 24.9% Score 236.5; DB 1; Length 304;  
 QY Best Local Similarity 34.9% Pred. No. 2e-15; Gaps 4;  
 QY Matches 53; Conservative 24; Mismatches 64; Indels 11; Gaps 4;  
 QY 9 DFLVSKVGRASMRWVNVTDGSCQLEVGGCDGSNNYLPEECLKCATVENA 68  
 Db 123 DCFLEEDPGIIRGYITRYFIMQSKOCERPKYGGCLGMMNFETLECKNTC--EDGL 179.  
 QY 69 TG ---DLATSRNAADSSVPSAPRQDSEDHSMDMNEYEYCTANAVTGPGRASPRWYF 124.  
 Db 180 NFGQVDNYGTQLNAVNS --QTP--QSTKVPSFFFHGPSMCLAPADRGICRANENRFYY 235  
 QY 125 DVERNSNNFTIWGCRONKNSVSEACMLRC 156  
 Db 236 NSVIGKCRPFKTSGGNNNNNTSKRECLRAC 267

Search completed: October 18, 2002, 10:34:09  
 Job time : 13 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model  
Run on: October 18, 2002, 10:33:48 ; Search time 17 Seconds  
(without alignments)  
960.893 Million cell updates/sec

Title: US-09-218-913D-52  
Perfect score: 948  
Sequence: 1 ADVERSITHDFCLVSKVVGRC.....ACMLRCFROQENPPLPLGSK 170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	658	69.4	252	JG0185	hepatocyte growth protein C37C3.6a [hypothetical prote
2	250.5	26.4	1558	2	alpha-1-microglobu
3	250.5	26.4	2167	2	hypothetical prote
4	249.5	26.3	352	1	alpha-1-microglobu
5	246.5	26.0	302	1	tissue factor path
6	244.5	25.8	123	2	inter-alpha-trypsi
7	244.5	25.8	352	1	alpha-1-microglobu
8	244	25.7	299	2	tissue factor path
9	243	25.6	300	2	lipoprotein-associ
10	242.5	25.6	337	1	alpha-1-microglobu
11	241.5	25.5	125	2	alpha-1-microglobu
12	240	25.3	2225	2	hypothetical prote
13	239.5	25.3	396	2	tissue factor path
14	237.5	25.1	349	2	alpha-1-microglobu
15	236.5	24.9	152089	1	tissue factor path
16	235.5	24.8	32264	2	alpha-1-microglobu
17	233.5	24.6	335708	2	tissue factor path
18	222	23.4	304	1	hypothetical prote
19	219	23.1	1043	2	hypothetical prote
20	214.5	22.6	922	2	hypothetical prote
21	210	22.2	235	2	tissue factor path
22	209	22.0	765	2	amplid precursor
23	208	21.9	1743	2	hypothetical prote
24	200	21.1	751	2	beta-amyloid precu
25	200	21.1	763	2	amyloid beta (A4)
26	199	21.0	1599	2	hypothetical prote
27	195	20.6	1522	2	protein T22F7.3 [
28	193.5	20.4	1391	2	hypothetical prote
29	193	20.4	1204	2	amyloid precursor
			1474	2	protein ZC84.6 [im

## ALIGNMENTS

RESULT 1						
JG0185	hepatocyte growth factor activator inhibitor type 2 - mouse					
C:Species: Mus musculus (house mouse)						
C:date: 23-Jul-199 #sequence_revision 23-Jul-1999 #text_change 11-May-2000						
C:Accession: JG0185						
R:Itto, H.; Kataoka, H.; Hamasuna, R.; Kitamura, N.; Koono, M.						
Biochem Biophys. Res. Commun. 255, 740-748, 1999						
A:Title Hepatocyte growth factor activator inhibitor type 2 lacking the first kunitz domain: animal Kunitz-type proteinase inhibitor homology <BPI>						
A:Reference number: JG0185; MUID:99160423						
A:Status: preliminary						
A: Molecule type: mRNA						
A:Residues: 1-252 <ITO>						
A:Cross references: GB:AF099016						
C:Superfamily: animal Kunitz-type proteinase inhibitor homology <BPI>						
F:133-133/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>						
Query Match 69.4%; Score 658; DB 2; Length 252;						
Best Local Similarity 68.2%; Pred. No. 9.6e-52; Mismatches 20; Gaps 0;						
Matches 116; Conservative 20; Mismatches 34; Indels 0; Gaps 0;						
Qy 1 ADERSIHDIFCLVSKVIVGRCRASMPRWYNYVTDGSCQLFVGGCDGNNSNNYLTKKECLKK 60						
Db 28 ASRELDVIESCGGSKVYKGCRASIPRWYNTIDGSCQPFVYGGCEGNGNNYQSKKECLDK 87						
Qy 61 CATVNTENATGDLATSRNAADSSVPSAPRQDSDHDSSDMNEYCYCTNANVYTPCRASFP 120						
Db 88 CAGYTENTDDNARNRNGADSSVLSVPKQSAEDLSAIFIENKECYCPKAVTGPCKRAFP 147						
Qy 121 RAYFDVENSNCNNFIYGCGRGKNNSYREEEACMLRCFTRQQENPPLPI/GSK 170						
Db 148 RWYDTERNSCISIYGGCGRGNRNSYLSQEACMOKHSGKQMPFLTGLK 197						
RESULT 2						
C89114 protein C37C3.6a [imported] - Caenorhabditis elegans						
C:Species: Caenorhabditis elegans						
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001						
C:Accession: C89114						
R:Anonymous, The C. elegans Sequencing Consortium.						
Science 282, 2012-2018, 1998						
A:Title Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating bio						
A:Reference number: A57000; MUID:9906613; PMID:9851916						
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/						
A:Note: Published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;						
A:Accession: C89114						
A:Status: preliminary						
A:Molecule type: DNA						
A:Residues: 1-1558 <STO>						
A:Cross references: GB:chr_V; PID:93294501; GSPDB:GN00023; CESP:C37C						



Query Match 26.08%; Pred. No. 9.3e-15; Score 246.5; DB 1; Length 302; Best Local Similarity 34.0%; Matches 54; Conservative 21; Mismatches 65; Indels 19; Gaps 3;

Qy 9 DFLVSKVGRCRASMPRWYNTDGSOLFVYGGCDGNNSNNYLTKKEELKKCA-TVTEEN 67  
Db 122 DFCFLEEDPGICRGMTRFYNNQSAPRQRDSEDHSSDMFNYEYCTANAVTGPGRCA 181

Qy 68 ATGDLATSR-----NAADSSVPSAPRQRDSEDHSSDMFNYEYCTANAVTGPGRCA 117  
Db 182 QKGDYVTNQITVTDRTTVNNVVIQATKAPSQWYDGPS-----WCLLEPADSGLCKA 233

Qy 118 SFRWYFQDVERNSCNNNFYGGCRGNKNSPSEACMLRC 156  
Db 234 SEKRFYYNPAIGKCRQFNNTYGGGNNNNNTKQDCNRC 277

RESULT 7  
HCHU  
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor [validated] - human  
N;Alternate names: bikinin; complex-forming glycoprotein heterogeneous in charge (HC)  
rich protein  
N;Contains: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor  
C;Species: Homo sapiens (man)  
C;Date: 15-Oct-1982 #sequence\_revision 30-Jun-1987 #text\_change 08-Dec-2000  
C;Accession: S13433; S10778; A93612; A90074; A90225; A90686; PNO450; B39079; A61580; 3217  
R;Vetr, H.; Gebhard, W.  
Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990  
R;Diarra-Nehrpour, M.; Bourguignon, J.; Sesbouee, R.; Saliot, J.P.; Leveillard, T.; M  
Eur. J. Biochem. 191, 131-139, 1990  
A;Title: Structure of the human alpha(1)-microglobulin-bikinin gene.  
A;Reference number: S13433; MUID:91214554  
A;Accession: S13433  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-352 <VET1>  
A;Cross-references: EMBL:X54816; PIDN:CAA18585; 1; PID:q825614; EMBL:X5481  
A;Title: Structural analysis of the human alpha(1)-microglobulin-bikinin  
A;Reference number: S10778; MUID:90336621  
A;Accession: S10778  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-202 <DI1A>  
R;Kaumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.  
Nucleic Acids Res. 14, 7839-7850, 1986  
A;Title: The mRNA for a protease inhibitor related to the HI-30 domain of inter-alpha-trypsin inhibitor  
A;Reference number: A93642; MUID:87040757  
A;Accession: A93642  
A;Molecule type: mRNA  
A;Residues: 1-352 <KAU>  
A;Cross-references: GB:X04494; PID:924478; PIDN:CAA28182; 1; PID:924479  
R;Lopez-Otin, C.; Grubb, A.O.; Mendez, E.  
Arch. Biochem. Biophys. 228, 544-554, 1984  
A;Title: The complete amino acid sequence of human complex-forming glycoprotein heter  
A;Reference number: A90074; MUID:9412649  
A;Accession: A90074  
A;Molecule type: protein  
A;Residues: 20-56,58-202 <L0P>  
A;Experimental source: individual with tubular proteinuria  
A;Note: no evidence of sequence heterogeneity could be found, in spite of persistent  
R;Takagi, T.; Takagi, K.; Kawai, T.  
Biochem. Biophys. Res. Commun. 98, 997-1001, 1981  
A;Title: Complete amino acid sequence of human alpha-1-microglobulin.  
A;Reference number: A9038; MUID:81184438  
A;Accession: A90225  
A;Molecule type: protein  
A;Residues: 20-47,58-136,138-141,'T',143-144,146-198 <TAK>  
A;Experimental source: pooled urine of patients with tubular proteinuria  
R;Atmanni, F.; Lacour, B.; Strecker, G.; Parvy, P.; Druet, M.  
R;Reisinger, P.; Hochstrasser, K.; Albert, G.J.; Lempart, K.; Salier, J.P.  
Biol. Chem. Hoppe-Seyler 366, 479-483, 1985  
A;Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood p  
A;Reference number: A90886; MUID:85225568  
A;Accession: A90886  
A;Molecule type: protein  
A;Residues: 206-290,'VI',293-342,'E',344-350 <REL>  
R;Eighild, J.J.; Salvesen, G.; Hefta, S.A.; Thogersen, I.B.; Rutherford, S.; Pizzo, S  
Biochem. Biophys. Res. Commun. 191, 1188-1195, 1993  
A;Title: Molecular characteristics of uronic-acid-rich protein  
A;Reference number: PNO450  
A;Accession: PNO450  
A;Molecule type: protein  
A;Residues: 206-211,'X' <ATM1>  
Qy 9 DFLVSKVGRCRASMPRWYNTDGSOLFVYGGCDGNNSNNYLTKKEELKKCA-TVTEEN 68  
Db 59 -----QACNLPIVRGCRAGIELWAEDAVK 83  
3 DSCQLGYSQGPCLGMFKRYGNTGSMACETFYGGCMGNFNSKECLQTETV--- 58

Query Match 25.8%; Pred. No. 5.5e-17; Score 244.5; DB 2; Length 123;  
Best Local Similarity 31.8%; Matches 47; Conservative 15; Mismatches 47; Indels 39; Gaps 1;

Qy 9 DFLVSKVGRCRASMPRWYNTDGSOLFVYGGCDGNNSNNYLTKKEELKKCA-TVTEEN 68  
Db 59 -----QACNLPIVRGCRAGIELWAEDAVK 83

Qy 129 NSCNNTIYGGCRGNKNSPSEACMLRC 156  
Db 84 GKCVRFIYGGCNGNGNQFQSKECKEKEYC 111

R; Chirat, F.; Balduyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J. Int. J. Biol. Chem. 23, 1201-1203, 1991  
A; Title: A chondroitin-sulfate chain is located on serine-10 of the urinary trypsin inhibitor. A; Reference number: A61580; MUID:92175157  
A; Accession number: A61580  
A; Molecule type: protein  
A; Residues: 214, 'X', 216-222, 'X'  
R; McKeehan, W.L.; Sakagami, Y.; Hoshi, H.; McKeehan, K.A. J. Biol. Chem. 261, 5378-5383, 1986  
A; Title: Two apparent human endothelial cell growth factors from human hepatoma cells are identical  
A; Reference number: A92583; MUID:86168278  
A; Accession number: B05604  
A; Molecule type: protein  
A; Residues: 206-214, 'X', 216-230, 'X', 232-239, 'X', 241-248, 'XX', 251-252, 'X', 254 <MCK>  
R; Englund, J.J.; Thgersen, T.B.; Pizzo, S.V.; Salveter, G. J. Biol. Chem. 264, 15975-15981, 1989  
A; Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-albumin  
A; Reference number: A92736; MUID:893380192  
A; Accession: C34245  
A; Molecule type: protein  
A; Residues: 206-225 <ENG2>  
R; Traboni, C.; Cortese, R. Nucleic Acids Res. 14, 6340, 1986  
A; Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobulin  
A; Reference number: A25303; MUID:86312901  
A; Accession: S0303  
A; Molecule type: mRNA  
A; Residues: 1-218, 'HW' <TRA>  
A; Note: this mRNA sequence appears to contain errors after residue 218  
R; Calero, M.; Escrivano, J.; Grubb, A.; Mendez, E. J. Biol. Chem. 269, 384-389, 1994  
A; Title: Location of a novel type of interpolyptide chain linkage in the human protein  
A; Reference number: A53110; MUID:94103241  
A; Accession: A53110  
A; Molecule type: protein  
A; Residues: 45-57 <CAL1>  
R; Yett, H.; Koegler, M.; Gebhard, W. FEBS Lett. 245, 137-140, 1989  
A; Title: The domain structure of the inhibitor subunit of human inter-alpha-trypsin inhibitor. A; Reference number: S03552; MUID:89171290  
A; Status: nucleic acid sequence not shown  
A; Molecule type: DNA  
A; Residues: 206-352 <VET>  
R; Malki, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Bourne Biol. Chem. 373, 1009-1018, 1992  
A; Title: Chondroitin sulfate covalently cross-links the three polypeptide chains of inter-alpha-trypsin inhibitor: their isolation  
A; Reference number: S28928; MUID:93039735  
A; Accession: S28930  
A; Status: preliminary  
A; Molecule type: protein  
A; Residues: 206-215 <MAL>  
R; Morelle, W.; Capon, C.; Balduyck, M.; Sautiere, P.; Kouach, M.; Michalski, C.; Bourne Eur. J. Biol. Chem. 221, 881-888, 1994  
A; Title: Chondroitin sulfate associated hyaluronan binding protein, forms a stable complex  
A; Reference number: A53642; MUID:94229087  
A; Accession: S43466  
A; Status: preliminary  
A; Molecule type: protein  
A; Residues: 206-221 <MOR>  
R; Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J. Biochemistry 33, 7423-7429, 1994  
A; Title: TSG-6, an arthritis-associated glycoprotein, forms a stable complex  
A; Reference number: A53642; MUID:94227199  
A; Accession: A53642  
A; Status: preliminary  
A; Molecule type: protein  
A; Residues: 206-217 <WIS>  
R; Calero, M.; Mendez, E.; Garcia, E. Biophys. Acta 1249, 91-99, 1995  
A; Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin) A; Reference number: S55688; MUID:95284116  
A; Accession: S55688

A; Molecule type: protein  
A; Residues: 20-24 <CAL2>  
R; Bourguignon, J.; Diarra-Mehrpoor, M.; Sesboue, R.; Frain, M.; Sala-Trepaut, J.M.; Mabiochem. Biophys. Res. Commun. 131, 116-115, 1985  
A; Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide sequence  
A; Reference number: I52208; MUID:86025577  
A; Accession: I52208  
A; Status: translated from GB/EMBL/DBJ  
A; Molecule type: mRNA  
A; Residues: 302-352 <BOU>  
A; Cross-references: GB:MI1562; PID:9186587; PID:AAA59194-1; PID:9307077  
R; Wojcik, F.G.C.; van den Berg, M.; van der Linden, I.K.; Cupers, R.; Be Biochem. J. 311, 753-759, 1995  
A; Title: Factor IX zutphien: a CYS(18) -> Arg mutation results in formation of a heterozygous protein  
A; Reference number: S559059; MUID:56067389  
A; Accession: S559059  
A; Molecule type: protein  
A; Residues: 27-35 'Y', 37 <WOJ>  
R; Attman, F.; Mizon, J.; Khan, S.R. Eur. J. Biochem. 236, 984-990, 1996  
A; Molecule type: protein  
A; Residues: 27-35 'Y', 37 <ATM2>  
R; Akerstrom, B.; Bratt, T.; Englund, J.J. FEBS Lett. 362, 50-54, 1995  
A; Title: Identification of uronic-acid-rich protein in urinary bikunin, the light chain of the alpha(1)-microglobulin chromophore in mammalian and insect  
A; Reference number: S663434; MUID:9627053  
A; Accession: S663434  
A; Molecule type: protein  
A; Residues: 206-214, 'X', 216-230 <ATM2>  
A; Title: Formation of the alpha(1)-microglobulin chromophore in mammalian and insect  
A; Reference number: S68728; MUID:95212582  
A; Accession: S68728  
A; Molecule type: protein  
A; Residues: 89-100 <AKA>  
R; Jessen, T.E.; Farver, K.H.; Ploug, M. FEBS Lett. 230, 195-200, 1988  
A; Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a structural study  
A; Reference number: S02431; MUID:88167187  
A; Accession: S02431  
A; Molecule type: protein  
A; Residues: 206-214, 'X', 216-217 <JES>  
R; Lopez, C.; Grubb, A.; Mendez, E. FEBS Lett. 141, 349-353, 1982  
A; Title: Human protein HC displays variability in its carboxyl-terminal amino acid sequence  
A; Reference number: A91304  
A; Contents: annotation; variant of alpha-1-microglobulin  
A; Note: pooled urine samples contained two forms of this protein, both lacking 57-Lys R; Hochstrasser, K.; Schonberger, O.L.; Rossmanith, I.; Wachter, E. Hoppe-Seyler's Z. Physiol. Chem. 362, 1357-1362, 1981  
A; Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inhibitor A; Note: in vitro, the first twelve residues of the inhibitor appear by affinity chromatography  
A; Content: annotation; A91698; MUID:82074265  
A; Content: annotation; carbohydrate binding sites R; Morii, M.; Travis, J. Biol. Chem. Hoppe-Seyler 366, 19-21, 1985  
C; Comment: Alpha-1-microglobulin occurs in many physiological fluids including plasma  
A; Title: The reactive site of human inter-alpha-trypsin inhibitor is in the amino-terminal region  
A; Reference number: A90682; MUID:85225540  
A; Contents: annotation; inhibitory site  
A; Note: in vitro, the first twelve residues of the inhibitor appear  
A; Status: preliminary  
A; Molecule type: protein  
A; Residues: 206-217 <WIS>  
R; Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J. Biochemistry 33, 7423-7429, 1994  
A; Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable complex  
A; Reference number: A53642; MUID:94227199  
A; Accession: A53642  
A; Status: preliminary  
A; Molecule type: protein  
A; Residues: 206-217 <WIS>  
R; Calero, M.; Mendez, E.; Garcia, E. Biophys. Acta 1249, 91-99, 1995  
A; Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin) A; Reference number: S55688; MUID:95284116  
A; Accession: S55688

Query 9 DECLVSKVYGRCRASMPRWNFTDGSCLFLVYGGCDGNNNNLYTKERLKKCATVTEA 68  
Db 229 DSGCGYSGPQGPMTSRKFQGCGMGNNVTEKEQLQTCRTVAA-- 286  
Query 69 TGDLATSRNAADSSVPSAARRQDSEHDSSDMFNEYCYCTANAVTGPGRASFPWMYEDVER 128  
Db 287 ----- 309

Qy	129	NSCNNFIYGGCRGNKNSYRSEBACMLRC 156	Best Local Similarity 30.0%;	Pred. No. 1.9e-14;	Matches 48;	Conservative 23;	Mismatches 61;	Indels 28;	Gaps 2;
Db	310	GRCVLFYGGCCQNGNKFYSECREVC 337							
<b>RESULT 8</b>									
I46937		tissue factor pathway inhibitor - rabbit							
C;Species: Oryctolagus cuniculus (domestic rabbit)									
C;Accession: I46937									
R;RelaxaquaJ A.; Kuppuswamy, M.N.; Birktoft, J.J.; Bajaj, S.P.									
Thromb. Res. 69, 547-553, 1993									
A;Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.									
A;Reference number: I46937; MUID:93276427									
A;Accession: I46937									
A;Status: preliminary; translated from GB/EMBL/DBJ									
A;Molecule type: mRNA									
A;Residues: 1-299 <BEL>									
A;Cross references: GB:S61902; PID:9186015; PID:AAH26836.1; PID:9386016									
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor									
C;Accession: S149-99									
F;120-1/0/Domain: animal Kunitz-type proteinase inhibitor homology <BP11>									
F;212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BP12>									
Query Match 25.78; Score 244; DB 2; Length 299;									
Best Local Similarity 30.0%;	Pred. No. 1.5e-14;	Matches 48;	Conservative 23;	Mismatches 61;	Indels 28;	Gaps 2;			
Qy	4	ERSIHDFCLVSKVGRCRASMRPWWNYNTDGSQCLFVYGGCDDNSNNYLTKEECLKKCAT 63							
Db	42	QKTHSFAAMKVDGPGRAYTKRFFFLTRQEEFYGGCNGNNEFESLECKERCAR 101							
Query Match 25.78; Score 244; DB 2; Length 299;									
Best Local Similarity 30.0%;	Pred. No. 1.5e-14;	Matches 48;	Conservative 23;	Mismatches 61;	Indels 28;	Gaps 2;			
Qy	64	VTENATGDLATSRNAADSSVPSAPRQDSEHSSDMENYEYCTANAVTGPGRASPRWY 123							
Db	102	DYPKMTIKLTKFGKPD-----FCFLEDPGICRGYTRYF 137							
Query Match 25.78; Score 244; DB 2; Length 299;									
Best Local Similarity 30.0%;	Pred. No. 1.5e-14;	Matches 48;	Conservative 23;	Mismatches 61;	Indels 28;	Gaps 2;			
Qy	64	ERSIHDFCLVSKVGRCRASMRPWWNYNTDGSQCLFVYGGCDDNSNNYLTKEECLKKCAT 63							
Db	138	YNNOSKOCERFRYGGCLGNLNNEFESLECKERNTC---ENP 173							
Query Match 25.78; Score 244; DB 2; Length 299;									
Best Local Similarity 30.0%;	Pred. No. 1.5e-14;	Matches 48;	Conservative 23;	Mismatches 61;	Indels 28;	Gaps 2;			
Qy	124	FDVERNSCNNFYGGCRGNKNSYRSEBACMLRCFQENP 163							
Db	138	YNNOSKOCERFRYGGCLGNLNNEFESLECKERNTC---ENP 173							
<b>RESULT 9</b>									
S12143		lipoprotein-associated coagulation inhibitor precursor - rabbit							
N;Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor									
C;Species: Oryctolagus cuniculus (domestic rabbit)									
C;Accession: I49-1997									
R;Wesselchmidt, R.L.; Girard, T.J.; Broze Jr., G.J.									
Nucleic Acids Res. 18, 6410, 1990									
A;Accession: S12143									
A;Status: preliminary									
A;Molecule type: mRNA									
A;Residues: 1-300 <W>									
A;Cross references: EMBL:X54708; PID:916121; PID:CAA38515.1; PID:91613									
R;Colburn, P.; Crabb, J.W.; Buonassisi, V.									
J. Cell. Physiol. 148, 320-326, 1991									
A;Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell									
A;Reference number: A61373; MUID:91349227									
A;Accession: A61373									
A;Molecule type: protein									
A;Residues: 25-33, 'X', 35-46 <COL>									
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor									
C;Keywords: anticoagulant; glycoprotein									
F;50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>;									
F;213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>;									
Query Match 25.6%; Score 243; DB 2; Length 300;									
Best Local Similarity 31.8%;	Pred. No. 2.4e-14;	Matches 19;	Conservative 19;	Mismatches 43;	Indels 39;	Gaps 1;			
Qy	9	DECLVSKVGRCRASMRPWWNYNTDGSQCLFVYGGCDDNSNNYLTKEECLKKCATYENA 68							
Db	214	DSCQQLGYSQGPOLGMKRYKFYNGSSWACETHYGGMNGNFSKECLQTCRTV--- 269							
Query Match 25.6%; Score 242.5; DB 1; Length 337;									
Best Local Similarity 31.8%;	Pred. No. 2.4e-14;	Matches 19;	Conservative 19;	Mismatches 43;	Indels 39;	Gaps 1;			
Qy	69	TGDLATSRNAADSSVPSAPRQDSEHSSDMENYEYCTANAVTGPGRASPRWYFDVER 128							

Db 270 -----BACSLPIVSGPCRGFFQLWAFDAVQ 294

Qy 129 NSCNNFYGCGNKNSYRSEACMLRC 156

Db 295 GRCVLFNYGGCGGNGNQFYSECKEKEYC 322

A; Molecule type: DNA

A; Residues: 1-225 &lt;WIL&gt;

A; Cross-references: EMBL:292815; PIDN:CA07294.1; GSPDB:GN00023; CESP:W01F3.3

A; Experimental source: clone W01F3

C; Genetics:

A; Gene: CESP:W01F3.3

A; Map position: 5

A; Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221

RESULT 11

T1H0B1 alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)

N; Alternate names: EI-14 (inhibitory fragment of ITI); ITI; trypsin inhibitor, E-UTI

C; Species: Equus caballus (domestic horse)

C; Date: 30-Jun-1997 #sequence\_revision 04-Feb-2000 #text\_change 05-May 2000

C; Accession: A01210; A45653

R; Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.

Biol. Chem. Hoppe-Seyler 366, 473-478, 1985

A; Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a

A; Reference number: A90685; MUID:85225967

A; Accession: A01210

A; Residues: 3-125 &lt;HOC&gt;

R; Veeraraghavan, K.; Singh, K.; Wachter, E.; Hochstrasser, K.

Biol. Chem. Int. 26, 405-413, 1992

A; Title: Characterization of a trypsin inhibitor from equine urine.

A; Reference number: A45653; MUID:92328813

A; Status: Preliminary

A; Molecule type: protein

A; Residues: 1-12, E, 14-33 &lt;VEED&gt;

A; Cross-references: PIDN:AB22430.0.1; PID:9250858

A; Experimental source: urine

A; Note: sequence extracted from NCBI backbone (NCBLP:107966)

C; Comment: This inhibitory fragment from native ITI after limited proteolysis

first domain interacts weakly with PMN-granulocytic elastase and not at all with pancreatic

C; Comment: The amino acid at position P2 (19-Met) appears to determine the specificity

C; elastase; those with leucine interact strongly.

C; Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology; lipocalin

C; Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor

C; PDB: 1-57/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP1&gt;

C; PDB: F63-113/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP2&gt;

C; PDB: F17/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted

C; PDB: F26/Binding site: carbohydrate (Asn) (covalent) #status experimental

C; PDB: F73/Inhibitory site: Arg (trypsin) #status predicted

Query Match Score 241.5; DB 1; Length 125;

Best Local Similarity 31.8%; Pred. No. 1e-14; Mismatches 15; Gaps 1;

Matches 47; Conservative 47; Indels 39; Gaps 1;

Query Match Score 241.5; DB 1; Length 125;

Best Local Similarity 31.8%; Pred. No. 1e-14; Mismatches 15; Gaps 1;

Matches 47; Conservative 24; Indels 60; Gaps 1;

Query Match Score 241.5; DB 1; Length 125;

Best Local Similarity 29.6%; Pred. No. 5.2e-14; Mismatches 45; Gaps 1;

Matches 45; Conservative 24; Indels 60; Gaps 1;

Query Match Score 241.5; DB 1; Length 125;

Best Local Similarity 29.6%; Pred. No. 5.2e-14; Mismatches 45; Gaps 1;

Matches 45; Conservative 24; Indels 60; Gaps 1;

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Matches 45; Conservative 24; Indels 60; Gaps 1;

Query Match Score 241.5; DB 1; Length 125;

Best Local Similarity 29.6%; Pred. No. 5.2e-14; Mismatches 45; Gaps 1;

Matches 45; Conservative 24; Indels 60; Gaps 1;

Query Match Score 241.5; DB 1; Length 125;

Best Local Similarity 29.6%; Pred. No. 5.2e-14; Mismatches 45; Gaps 1;

Matches 45; Conservative 24; Indels 60; Gaps 1;

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Best Local Similarity 29.6%; Pred. No. 5.2e-14; Mismatches 45; Gaps 1;

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Query Match Score 241.5; DB 1; Length 125;

Best Local Similarity 29.6%; Pred. No. 5.2e-14; Mismatches 45; Gaps 1;

Matches 45; Conservative 24; Indels 60; Gaps 1;

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Matches 45; Conservative 24; Indels 60; Gaps 1;

Query Match Score 241.5; DB 1; Length 125;

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Matches 45; Conservative 24; Indels 60; Gaps 1;

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Query Match Score 241.5; DB 1; Length 125;

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Matches 45; Conservative 24; Indels 60; Gaps 1;

Query Match Score 241.5; DB 1; Length 125;

Best Local Similarity 29.6%; Pred. No. 5.2e-14; Mismatches 45; Gaps 1;

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Best Local Similarity 29.6%; Pred. No. 5.2e-14; Mismatches 45; Gaps 1;

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Best Local Similarity 29.6%; Pred. No. 5.2e-14; Mismatches 45; Gaps 1;

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Best Local Similarity 29.6%; Pred. No. 5.2e-14; Mismatches 45; Gaps 1;

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Best Local Similarity 29.6%; Pred. No. 5.2e-14; Mismatches 45; Gaps 1;

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Best Local Similarity 29.6%; Pred. No. 5.2e-14; Mismatches 45; Gaps 1;

Matches 45; Conservative 24; Indels 60; Gaps 1;

Query Match Score 241.5; DB 1; Length 125;

Best Local Similarity 29.6%; Pred. No. 5.2e-14; Mismatches 45; Gaps 1;

Matches 45; Conservative 24;

A; Reference number: S21089; MUID: 92182014  
 A; Accession: S21089  
 A; Status: preliminary  
 A; Molecule type: mRNA  
 A; Residues: 1-349 <LIN>  
 A; Cross-references: GB:S87544; NID:9247162; PID:9247163  
 A; Residues: 1-349 <LIN>  
 A; Cross-references: GB:S73337; NID:9685016; PIDN: AAB31955.1; MUID: 94375417  
 A; Reference number: JC2364  
 A; Accession: JC2364  
 A; Molecule type: mRNA  
 A; Residues: 1-304 <KAM>  
 A; Cross-references: GB:S73337; NID:9685016; PID:9685017  
 A; Experimental source: liver  
 A; Residues: 1-304 <KAM>  
 A; Comment: This protein inhibits the activities of factor Xa and tissue factor-factor  
 C; Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor  
 C; Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor  
 F: 1-28/Domain: signal sequence #status predicted <SIG>  
 F: 29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>  
 F: 54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
 F: 125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
 F: 211-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>  
 F: 54-104/63-87/Domain: animal Kunitz-type proteinase inhibitor homology <BP4>  
 F: 125-175/100-125-158/150-171-217-267/226-250-242-263/Disulfide bonds  
 F: 64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted  
 F: 135/Inhibitory site: Arg (coagulation factor X) #status predicted  
 F: 145-195/256/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F: 227/Inhibitory site: Arg (unidentified proteinase) #status predicted

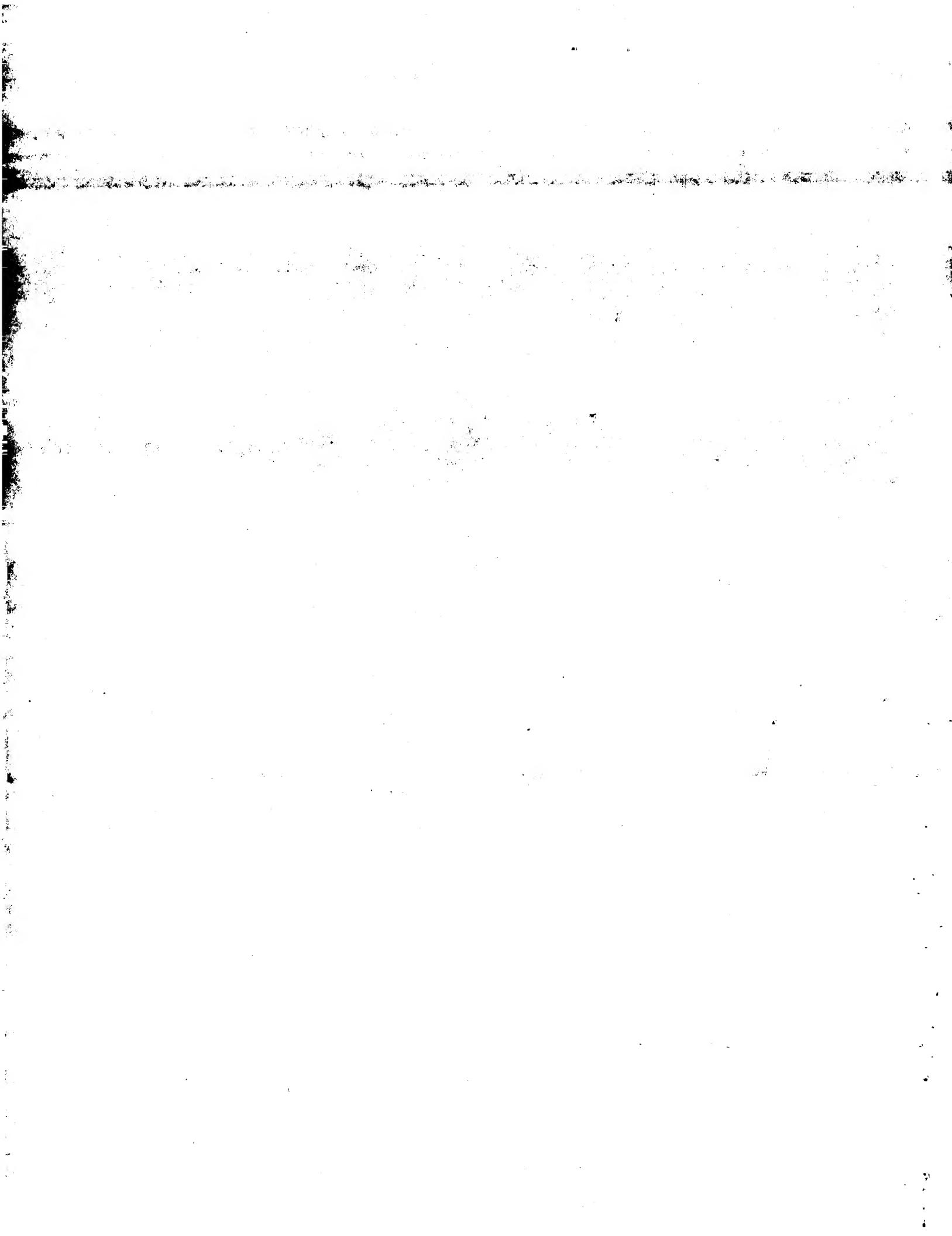
Query Match 24.9%; Score 236.5; DB 1; Length 304;  
 Best Local Similarity 34.9%; Pred. No. 7.4e-14;  
 Matches 53; Conservative 24; Mismatches 64; Indels 11; Gaps 4;

Qy 9 DFLCLSKVVRGRASMRWVNTDGSCLQFLVGGDGNSNNYLRECLKKCATVTEA 68  
 Db 123 DFCFLEEDPGICRGYITRYFVNNQSOKCERFYGGCLGNMNNFETLGECKNTC -- EDGL 179  
 Qy 69 TG --- DIAITRSNAADSSVPSAPRQDSHDSSDMFNEYENCTANAVTGPGRASFPWYF 124  
 Db 180 NGFQVDNYGTOLNAVNS -- QTPP--QSTKVSSEFFHGPSPNCLAPDRGLCRANENRYY 235  
 C; Superfamily: 205-213/215-229/215-229/215-229/215-229/231-232/231-232/231-232/234-238 <SUG>  
 R; Sugiki, M.; Maruyama, M.; Yoshida, E.; Sumi, H.; Miura, H.  
 Inflammation 15, 281-289, 1991  
 A; Title: Acid-stable protease inhibitor in chronic phase of carrageenin-induced inflamma  
 A; Reference number: A31890; MUID: 89053978  
 A; Accession: A31890  
 A; Molecule type: protein  
 A; Residues: 283-301, 'L', 303-322, 'N', 324-329, 'PK', 332-333, 'W', 335-343 <KTD>  
 R; Sugiki, M.; Maruyama, M.; Yoshida, E.; Sumi, H.; Miura, H.  
 Inflammation 15, 281-289, 1991  
 A; Title: Acid-stable protease inhibitor in chronic phase of carrageenin-induced inflamma  
 A; Reference number: A61633; MUID: 92120777  
 A; Accession: A61633  
 A; Molecule type: protein  
 A; Residues: 205-213/215-229/215-229/215-229/231-232/231-232/231-232/234-238 <SUG>  
 C; Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology; lipocalin  
 C; Superfamily: chondroitin sulfate proteoglycan; chondroitin; glycoprotein; plasma; serin  
 F: 1-19/Domain: signal sequence #status predicted <SIG>  
 F: 20-202/Product: alpha-1-microglobulin #status predicted <ALM>  
 F: 44-187/Domain: lipocalin homology <LIP>  
 F: 205-249/Product: inter-alpha-trypsin inhibitor #status experimental <TAI>  
 F: 230-280/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
 F: 74/Binding site: chondroitin sulfate proteoglycan; chondroitin; glycoprotein; plasma; serin  
 F: 52/Cross-link: alpha-1-microglobulin-Ig alpha complex chromophore (Cys) (interchain to  
 F: 214/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted  
 F: 296/Inhibitory site: Arg (trypsin) #status predicted

Query Match 25.1%; Score 237.5; DB 2; Length 349;  
 Best Local Similarity 30.4%; Pred. No. 6.9e-14;  
 Matches 45; Conservative 17; Mismatches 47; Indels 39; Gaps 1;

Qy 9 DFLCLSKVVRGRASMRWVNTDGSCLQFLVGGDGNSNNYLRECLKKCATVTEA 68  
 Db 228 DSCQLNNTSEGPCIGMQQQKYINGASMACETFGYGGCLGNMNNFASEKECLCRTCIAA-- 285  
 Qy 69 TGDLTATRSNAADSSVPSAPRQDSHDSSDMFNEYENCTANAVTGPGRASPRWYDVER 128  
 Db 286 ---CNLPITVQGBCRAFAELWAAQ 308  
 Qy 129 NSCNCNNFIYGGCRRGNKNSYRSEFACMLRC 156  
 Db 309 GRCIOFIFYGGCRRGNKNSYRSEFECKEYC 336

RESULT 15  
 JC2264  
 tissue factor pathway inhibitor precursor - rhesus macaque  
 N; Alternative names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib  
 C; Species: Macaca mulatta (rhesus macaque)  
 C; Date: 10-Sep-1999 #sequence\_change 10-Sep-1999 #text\_change 21-Jul-2000  
 C; Accession: JC2264



SUMMARIES			
Result No.	Score	Query Match	Length DB ID
1	948	100.0	170 18 AAW30041
2	948	100.0	170 21 AAB14189
3	948	100.0	170 21 AAB14190
4	948	100.0	179 18 AAB30053
5	948	100.0	179 21 AAB14159
6	948	100.0	197 18 AAW30043
7	948	100.0	197 21 AAB14160
8	948	100.0	213 18 AAW30042
9	948	100.0	213 21 AAB14184
10	948	100.0	213 21 AAB14200
11	948	100.0	225 18 AAW30046

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

XX New human placental bikunin - used to inhibit kallikrein, trypsin  
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or  
 PR perioperative blood loss  
 XX

PS Claim 1; Page 65; 110pp; English.

XX The present sequence is a human placental bikunin, which  
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.  
 CC Bikunin can be used to treat or prevent brain and spinal cord  
 CC oedema, inflammation, infection or granulomatosis, multiple  
 CC scleroses, ischaemia, perioperative diseases, polytrauma, stroke,  
 CC fibrosis, blood coagulation diseases, cerebral or subarachnoid hemorrhage and gastric or cervical  
 CC cancer and prevent metastasis. It is particularly useful for  
 CC reducing blood loss during surgery, and can also be used to treat  
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,  
 CC influenza and similar viral infections, acute pancreatitis and  
 CC gout, and prevent pre term labour. It has similar properties to  
 CC plasmin, but is less highly charged so should be less  
 CC immunogenic and less likely to damage the kidneys. Manipulation  
 CC of the bikunin sequence may allow the inhibitory profile to be  
 CC altered. It also reduces or eliminates the need for whole donor  
 CC blood or blood products during surgery, thereby reducing the risk  
 CC of infection and other adverse side effects, as well as reducing  
 CC the cost of surgery.  
 XX

Sequence 170 AA;

Query Match 100.0%; Score 948; DB 18; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 4e-89;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADVERS1HDFCLVSKVYGRCA1SMPPWYNTDGSCQLFYGGCDGNSNNYLTKEECLKK 60  
 Db 1 ADERS1HDFCLVSKVYGRCA1SMPPWYNTDGSCQLFYGGCDGNSNNYLTKEECLKK 60

QY 61 CATVTEENATGDLATSRNAADSSVPSAPRQDSEDHSSDMENYEYCTANAVTGPGRASFP 120  
 Db 61 CATVTEENATGDLATSRNAADSSVPSAPRQDSEDHSSDMENYEYCTANAVTGPGRASFP 120

QY 121 RWYFDVERNSCNMFYGGCRNKNSYRSEEACMLRCFQQENPPLPLGSK 170  
 Db 121 RWYFDVERNSCNMFYGGCRNKNSYRSEEACMLRCFQQENPPLPLGSK 170

RESULT 2  
 AAB14189 standard; protein; 170 AA.  
 XX AAB14189;  
 AC AAB14189;  
 XX DT 02-FEB-2001 (first entry)  
 XX DE Human Placental bikunin protein # 7.  
 KW Human; mucociliary dysfunction; mucus; sputum;  
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;  
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;  
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.  
 OS Homo sapiens.  
 XX PN WO20037099-A2.  
 XX PD 29-JUN-2000.  
 XX PF 22-DEC-1999; 99WO-GB04381.  
 XX PR 22-DEC-1998; 98US-0218913.  
 XX PR 17-NOV-1999; 99US-0441966.  
 XX PR (FARB ) BAYER AG.

XX Hall R, Poll CT, Newton BB, Taylor WJA;  
 PT XX WPI; 2000-452127/39.  
 PT XX Stimulating mucociliary clearance rate of mucus and sputum in lung  
 PT airways for treating lung diseases such as cystic fibrosis and  
 PT bronchitis involves administering a Kunitz-type serine protease  
 PT inhibitor -  
 XX Disclosure; Pages 166-167; 173pp; English.

XX Mucociliary dysfunction is the inability of ciliated epithelium to clear  
 CC mucus and sputum in lung airways. Mucociliary dysfunction such as Chronic  
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).  
 CC In addition, patients suffering from mucociliary dysfunction are  
 CC susceptible to secondary bacterial infections. The present sequence is  
 CC a sequence for human Placental bikunin protein. This sequence was  
 CC derived from a human placental cDNA library by PCR-based amplification.  
 CC This protein is a Kunitz-type serine protease inhibitor protein, which  
 CC can stimulate the rate of mucociliary clearance of mucus and sputum in  
 CC lung airways. Therefore, the present protein may be used for treating  
 CC lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear.  
 CC Note: the present sequence is defined as SEQ ID 51 in the sequence  
 CC listing. However, in figure 4C of the specification, SEQ ID 51 is  
 CC clearly shown as a nucleotide sequence. Therefore, the nucleotide  
 CC sequence has been described in AIA70392.

XX SQ Sequence 170 AA;

Query Match 100.0%; Score 948; DB 21; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 4e-89.  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADRESRSTHDFLCLVSKVYGRCA1SMPPWYNTDGSCQLFYGGCDGNSNNYLTKEECLKK 60  
 Db 1 ADERS1HDFCLVSKVYGRCA1SMPPWYNTDGSCQLFYGGCDGNSNNYLTKEECLKK 60

QY 61 CATVTEENATGDLATSRNAADSSVPSAPRQDSEDHSSDMENYEYCTANAVTGPGRASFP 120  
 Db 61 CATVTEENATGDLATSRNAADSSVPSAPRQDSEDHSSDMENYEYCTANAVTGPGRASFP 120

QY 121 RWYFDVERNSCNMFYGGCRNKNSYRSEEACMLRCFQQENPPLPLGSK 170  
 Db 121 RWYFDVERNSCNMFYGGCRNKNSYRSEEACMLRCFQQENPPLPLGSK 170

RESULT 3  
 AAB14190  
 ID AAB14190 standard; protein; 170 AA.  
 XX AC AAB14190;  
 XX DT 02-FEB-2001 (first entry)  
 XX DE Human placental bikunin protein # 8.  
 KW Human; mucociliary dysfunction; mucus; sputum;  
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;  
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;  
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.  
 XX OS Homo sapiens.  
 XX PN WO20037099-A2.  
 XX PD 29-JUN-2000.  
 XX PF 22-DEC-1999; 99WO-GB04381.  
 XX PR 22-DEC-1998; 98US-0218913.  
 XX PR 17-NOV-1999; 99US-0441966.  
 XX PR (FARB ) BAYER AG.

PR	17-NOV-1999;	99US-0441966.
XX	XX	
PA	(FARB ) BAYER AG.	
XX	PA	
PI	Hall R, Poll CT, Newton BB, Taylor WJA;	
XX	PT	
PT	Stimulating mucociliary clearance rate of mucus and sputum in lung airways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease inhibitor	
XX	PT	
PT	WPI; 2000-452127/39.	
XX	DR	
PS	Claim 14; Page 90; 173pp; English.	
XX	CC	Mucociliary dysfunction is the inability of ciliated epithelium to clear mucus and sputum in lung airways. Mucociliary dysfunction is a serious complication of chronic obstructive lung diseases such as Chronic Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF). In addition, patients suffering from mucociliary dysfunction are susceptible to secondary bacterial infections. The present sequence is a sequence for human placental bikunin protein. This sequence was derived from a human placental cDNA library by PCR-based amplification. This protein is a Kunitz-type serine protease inhibitor protein, which can stimulate the rate of mucociliary clearance of mucus and sputum in lung airways. Therefore, the present protein may be used for treating lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are caused by retention and accumulation of mucus.
XX	SQ	Sequence 170 AA:
XX	Query Match 100 0%; Score 948; DB 21; Length 170;	
XX	Best Local Similarity 100 0%; Pred. No. 4e-89;	
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 ADRESIHDCLVSKVGVGRASMRPRWNVTDGSCOLFYGGCDGNSNNYLKEECLKK 60	
Db	1 ADRESIHDCLVSKVGVGRASMRPRWNVTDGSCOLFYGGCDGNSNNYLKEECLKK 60.	
QY	61 CATYENATDLATRNAAASSVSPAPRQDSEDISSDMNEYEECTANAVTGPGRASFP 120	
Db	61 CATYENATDLATRNAAASSVSPAPRQDSEDISSDMNEYEECTANAVTGPGRASFP 120	
QY	121 RWYDVERNSCNNFTYGGCNGKNSYRSEBACMLRCFQROENPPLPLGSK 170	
Db	121 RWYDVERNSCNNFTYGGCNGKNSYRSEBACMLRCFQROENPPLPLGSK 170	
RESULT 4		
ID	AAW30053	standard; Protein: 179 AA.
XX	AAW30053	
AC	AAW30053;	
XX	DT 20-APR-1998	(first entry)
XX	XX	Human Placental bikunin.
XX	KW	Human; placental bikunin; inhibition; trypsin; kallikrein; plasmin; factor XIIa; treatment; prevention; oedema; inflammation; infection; granulomatosis; multiple sclerosis; ischaemia; perioperative blood loss; sepsis; shock; fibrosis; blood coagulation disease; polytrauma; stroke; haemorrhage; gastric cancer; cervical cancer; metastasis; blood loss.
XX	OS	Homo sapiens.
XX	PN	WO9733996-A2.
XX	PD	18-SEP-1997.
XX	PF	10-MAR-1997.
XX		

XX	29-JUN-2000.	PN	W09733996-A2
XX		XX	
PD	22-DEC-1999;	PD	18-SEP-1997.
PF	99WO-GB04381.	XX	
XX		PF	10-MAR-1997;
PR	22-DEC-1998;	XX	97WO-US03894.
PR	17-NOV-1999;	PR	04-OCT-1996;
PR	99US-0441966.	PR	96US-0725251.
XX		PR	11-MAR-1996;
PA	(FARB ) BAYER AG	PR	14-JUN-1996;
XX		XX	96US-0013106.
PA		XX	96US-0019793.
PI	Hall R, Poll CT, Newton BB, Taylor WJA;	PA	(FARB ) BAYER CORP.
XX		XX	
DR	WPI: 2000-452127/39.	PI	Davies G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX		XX	
PT	Stimulating mucociliary clearance rate of mucus and sputum in lung	DR	WPI: 1997-470876/43.
PR	airways for treating lung diseases such as cystic fibrosis and	XX	
PR	bronchitis involves administering a Kunitz-type serine protease	PT	New human placental bikunin - used to inhibit kallikrein, trypsin
PR	inhibitor -	PT	etc. in treatment of oedema, multiple sclerosis, fibrosis, or
XX		PT	perioperative blood loss
PS	Claim 14: Pages 89-90; 173pp; English.	XX	
XX		PS	Claim 1; Page 65; 110pp; English.
CC	Mucociliary dysfunction is the inability of ciliated epithelium to clear	XX	XX
CC	mucus and sputum in lung airways. Mucociliary dysfunction is a serious	CC	The present sequence is a human placental bikunin, which
CC	complication of chronic obstructive lung diseases such as Chronic	CC	inhibits, e. g. trypsin, kallikrein, plasmin and factor XIIA.
CC	Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).	CC	Bikunin can be used to treat or prevent brain and spinal cord
CC	In addition, patients suffering from mucociliary dysfunctions are	CC	oedema, inflammation, infection or granulomatosis, multiple
CC	susceptible to secondary bacterial infections. The present sequence is	CC	sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC	human placental bikunin. This protein is a Kunitz-type serine protease	CC	fibrosis, blood coagulation diseases, polytrauma, stroke,
CC	protein, which can stimulate the rate of mucociliary clearance	CC	cerebral or subarachnoid haemorrhage and gastric or cervical
CC	of mucus and sputum in lung airways. Therefore, the present protein may	CC	cancer and prevent metastasis. It is particularly useful for
CC	be used for treating lung diseases such as CF, CB, BE, and chronic	CC	reducing blood loss during surgery and can also be used to treat
CC	sinusitis and glue ear which are caused by retention and accumulation of	CC	other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC	mucus. The present sequence is the mature human placental	CC	influenza and similar viral infections, acute pancreatitis and
CC	protein. The present sequence is the mature human placental	CC	gout, and prevent pre-term labour. It has similar properties to
CC	sequence.	CC	aprotinin, but is less highly charged so should be less
CC		CC	immunogenic and less likely to damage the kidneys. Manipulation
CC		CC	of the bikunin sequence may allow the inhibitory profile to be
CC		CC	altered. It also reduces the need for whole donor
CC		CC	blood or blood products during surgery, thereby reducing the risk
CC		CC	of infection and other adverse side effects, as well as reducing
XX		XX	the cost of surgery.
SQ	Sequence 179 AA;	SQ	Sequence 197 AA;
Query	Query Match 100.0%; Score 948; DB 21; Length 197;	Query	Query Match 100.0%; Score 948; DB 18; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.2e-89;	Best Local Similarity 100.0%; Pred. No. 4.8e-19;	Best Local Similarity 100.0%; Pred. No. 4.8e-19;	Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 170; Conservative 0; Mismatches 0; Gaps 0;	Matches 170; Conservative 0; Mismatches 0; Gaps 0;	Matches 170; Conservative 0; Mismatches 0; Gaps 0;	Matches 170; Conservative 0; Mismatches 0; Gaps 0;
Qy 1 ADERSIHDIFCLVSKVGRCRASMPRKWNYTDGSCLFVGGCDNSNNYLTKEBCLKK 60	Qy 1 ADERSIHDIFCLVSKVGRCRASMPRKWNYTDGSCLFVGGCDNSNNYLTKECCLKK 60	Qy 1 ADERSIHDIFCLVSKVGRCRASMPRKWNYTDGSCLFVGGCDNSNNYLTKECCLKK 60	Qy 1 ADERSIHDIFCLVSKVGRCRASMPRKWNYTDGSCLFVGGCDNSNNYLTKECCLKK 60
Db 1 ADERSIHDIFCLVSKVGRCRASMPRKWNYTDGSCLFVGGCDNSNNYLTKEBCLKK 60	Db 19 ADERSIHDIFCLVSKVGRCRASMPRKWNYTDGSCLFVGGCDNSNNYLTKEBCLKK 78	Db 19 ADERSIHDIFCLVSKVGRCRASMPRKWNYTDGSCLFVGGCDNSNNYLTKEBCLKK 78	Db 19 ADERSIHDIFCLVSKVGRCRASMPRKWNYTDGSCLFVGGCDNSNNYLTKEBCLKK 78
Qy 61 CATVTEENATGDLATSRNAADSSVPSAFRQDSEHDSSDMFNEYEYCTANAVTGPCRASFP 120	Qy 61 CATVTEENATGDLATSRNAADSSVPSAFRQDSEHDSSDMFNEYEYCTANAVTGPCRASFP 120	Qy 61 CATVTEENATGDLATSRNAADSSVPSAFRQDSEHDSSDMFNEYEYCTANAVTGPCRASFP 120	Qy 61 CATVTEENATGDLATSRNAADSSVPSAFRQDSEHDSSDMFNEYEYCTANAVTGPCRASFP 120
Db 61 CATVTEENATGDLATSRNAADSSVPSAFRQDSEHDSSDMFNEYEYCTANAVTGPCRASFP 120	Db 79 CATVTEENATGDLATSRNAADSSVPSAFRQDSEHDSSDMFNEYEYCTANAVTGPCRASFP 138	Db 79 CATVTEENATGDLATSRNAADSSVPSAFRQDSEHDSSDMFNEYEYCTANAVTGPCRASFP 138	Db 79 CATVTEENATGDLATSRNAADSSVPSAFRQDSEHDSSDMFNEYEYCTANAVTGPCRASFP 138
Qy 121 RWYFDVERNSCNINFYGGCRGNKNSRSEEACMLRCRQENPPLIGSK 170	Qy 121 RWYFDVERNSCNINFYGGCRGNKNSRSEEACMLRCRQENPPLIGSK 170	Qy 121 RWYFDVERNSCNINFYGGCRGNKNSRSEEACMLRCRQENPPLIGSK 170	Qy 121 RWYFDVERNSCNINFYGGCRGNKNSRSEEACMLRCRQENPPLIGSK 170
Db 121 RWYFDVERNSCNINFYGGCRGNKNSRSEEACMLRCRQENPPLIGSK 170	Db 139 RWYFDVERNSCNINFYGGCRGNKNSRSEEACMLRCRQENPPLIGSK 188	Db 139 RWYFDVERNSCNINFYGGCRGNKNSRSEEACMLRCRQENPPLIGSK 188	Db 139 RWYFDVERNSCNINFYGGCRGNKNSRSEEACMLRCRQENPPLIGSK 188
RESULT 6			
AAW30043			
ID AAW30043 standard; Protein: 197 AA.			
XX			
AC AAW30043;			
XX			
DE 20-APR-1998 (first entry)			
XX			
DE Human placental bikunin.			
XX			
KW Human; placental bikunin; inhibition; trypsin; kallikrein;			
KW plasmin; factor XIIA; treatment; prevention; oedema;			
KW inflammation; infection; granulomatosis; multiple sclerosis;			
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;			
KW blood coagulation disease; polytrauma; stroke; haemorrhage;			
KW gastric cancer; cervical cancer; metastasis; blood loss.			
XX			
KW Human; mucociliary dysfunction; mucus; sputum;			
KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;			
OS Homo sapiens.			
XX			

KW	BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;	XX	Human placental bikunin.
XX	Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.	XX	
OS		XX	
OS	Homo sapiens.	XX	
FH	Location/Qualifiers	XX	
FT	1..18	XX	Human; placental bikunin; inhibition; trypsin; kallikrein; plasmin; factor XIIa; treatment; prevention; oedema; inflammation; infection; granulomatosis; multiple sclerosis; ischaemia; perioperative blood loss; sepsis; shock; fibrosis; blood coagulation disease; polytrauma; stroke; haemorrhage; gastric cancer; cervical cancer; metastasis; blood loss.
FT	/label= Signal_peptide	XX	
FT	1..19	XX	
FT	/label= Mature_protein	XX	
XX	WO2000037099-A2.	OS	
PN		OS	Homo sapiens.
PD	29-JUN-2000.	XX	
XX		XX	
PF	22-DEC-1999; 99WO-GB04381.	XX	
XX		XX	
PR	22-DEC-1998; 98US-0218913.	XX	
PR	17-NOV-1999; 99US-0441966.	XX	
XX		XX	
PA	(FARB ) BAVER AG.	XX	
XX		XX	
PI	Hall R, Poll CT, Newton BB, Taylor WJA;	XX	
XX		XX	
DR	WPI: 2000-452127/39.	XX	
XX		XX	
PT	Stimulating mucociliary clearance rate of mucus and sputum in lung airways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease inhibitor	XX	
PT		XX	
PT	Claim 13; Page 88; 173pp; English.	XX	
XX		XX	
CC	Mucociliary dysfunction is the inability of ciliated epithelium to clear mucus and sputum in lung airways. Mucociliary dysfunction is a serious complication of chronic obstructive lung diseases such as Chronic Bronchitis (CB). Bronchiectasis (BE), asthma and Cystic Fibrosis (CF). In addition, patients suffering from mucociliary dysfunction are susceptible to secondary bacterial infections. The present sequence is human placental bikunin. This protein is a Kunitz-type serine protease inhibitor protein, which can stimulate the rate of mucociliary clearance of mucus and sputum in lung airways. Therefore, the present protein may be used for treating lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are caused by retention and accumulation of mucus. The present sequence is the full-length human placental bikunin protein sequence.	XX	
XX	Sequence 197 AA;	XX	
SQ	Query Match 100.0%; Score 94B; DB 21; Length 197; Best Local Similarity 100.0%; Pred. No. 4.8e-89; Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	
Qy	1 ADRESSTHDFCLVSKVGRCAASMRPWWYNTDGSQLFVYGCDDNSNNYLTKEBCLKK 60	Qy	1 ADRESSTHDFCLVSKVGRCAASMRPWWYNTDGSQLFVYGCDDNSNNYLTKEECLKK 60
Db	19 ADRESSTHDFCLVSKVGRCAASMRPWWYNTDGSQLFVYGCDDNSNNYLTKEBCLKK 78	Db	1 ADRESSTHDFCLVSKVGRCAASMRPWWYNTDGSQLFVYGCDDNSNNYLTKEECLKK 60
Qy	61 CATVTENATGDLATSRNAADSSVPSAPRQDSEDDISDMNEYEECTANAVTGPGRASFP 120	Qy	1 CATVTENATGDLATSRNAADSSVPSAPRQDSEDDISDMNEYEECTANAVTGPGRASFP 120
Db	79 CATVTENATGDLATSRNAADSSVPSAPRQDSEDDISDMNEYEECTANAVTGPGRASFP 138	Db	1 ADRESSTHDFCLVSKVGRCAASMRPWWYNTDGSQLFVYGCDDNSNNYLTKEECLKK 60
Qy	121 RWYFDVERNSCNINFYGGCRGNKNSYRSEEFACMLRCFQQENPPLPLGSK 170	Qy	61 CATVTENATGDLATSRNAADSSVPSAPRQDSEDDISDMNEYEECTANAVTGPGRASFP 120
Db	139 RWYFDVERNSCNINFYGGCRGNKNSYRSEEFACMLRCFQQENPPLPLGSK 188	Db	61 CATVTENATGDLATSRNAADSSVPSAPRQDSEDDISDMNEYEECTANAVTGPGRASFP 120
RESULT 8		Qy	121 RWYFDVERNSCNINFYGGCRGNKNSYRSEEFACMLRCFQQENPPLPLGSK 170
ID AAW30042	standard; Protein; 213 AA.	AC	AAW30042; first entry
XX		XX	
AC		XX	
DT	20-APR-1998	DT	

RESULT 9  
 AAB14184 ID AAB14184 standard; protein; 213 AA.  
 XX  
 AC AAB14184;  
 XX  
 DT 02-FEB-2001 (first entry)  
 XX Human placental bikunin protein # 2.  
 XX Human; mucociliary dysfunction; mucus; sputum;  
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;  
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;  
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.  
 XX Homo sapiens.  
 XX WO200037099-A2.  
 XX PD 29-JUN-2000.  
 XX PF 22-DEC-1999; 99WO-GB04381.  
 XX PR 22-DEC-1998; 98US-0218913.  
 XX PR 17-NOV-1999; 99US-0441966.  
 XX PA (FARB ) BAYER AG.  
 XX PI Hall R, Poll CT, Newton BB, Taylor WJA;  
 XX DR 2000-452127/39.  
 XX PT Stimulating mucociliary clearance rate of mucus and sputum in lung  
 PT airways for treating lung diseases such as cystic fibrosis and  
 PT bronchitis involves administering a Kunitz-type serine protease  
 PT inhibitor.  
 XX PS Disclosure; Page 162; 173pp; English.  
 XX CC Mucociliary dysfunction is the inability of ciliated epithelium to clear  
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious  
 CC complication of chronic obstructive lung diseases such as Chronic  
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).  
 CC In addition, patients suffering from mucociliary dysfunction are  
 CC susceptible to secondary bacterial infections. The present sequence is a  
 CC fragment of human placental bikunin. Human placental bikunin is a  
 CC Kunitz-type serine protease inhibitor protein, which can stimulate the  
 CC rate of mucociliary clearance of mucus and sputum in lung airways.  
 CC Therefore, the present protein fragment may be used for treating lung  
 CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which  
 CC are caused by retention and accumulation of mucus.  
 CC Note: the present sequence is defined as SEQ ID 46 in the sequence  
 CC listing. In figure 4E of the specification, SEQ ID 46 is  
 CC clearly shown as a nucleotide sequence. Therefore, the nucleotide  
 CC sequence has been described in AAA70393.  
 XX SQ Sequence 213 AA;  
 Query Match 100.0%; Score 948; DB 21; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-89;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADRESS1HDFCLVSKVVGCRASMPRWYNTDGSQLFVYGGCDGNSNNYLTKEBCLKK 60  
 Db 1 ADRESS1HDFCLVSKVVGCRASMPRWYNTDGSQLFVYGGCDGNSNNYLTKEBCLKK 60  
 QY 61 CATVTEENATGDLATSRNAADSSVPSAPRQDSEHDSSDMFNEYCTANAVTGPGRASFP 120  
 Db 61 CATVTEENATGDLATSRNAADSSVPSAPRQDSEHDSSDMFNEYCTANAVTGPGRASFP 120  
 QY 61 CATVTEENATGDLATSRNAADSSVPSAPRQDSEHDSSDMFNEYCTANAVTGPGRASFP 120  
 Db 61 CATVTEENATGDLATSRNAADSSVPSAPRQDSEHDSSDMFNEYCTANAVTGPGRASFP 120  
 QY 121 RWYFDVERNSCNNF1YGGCRGNKNSYRSEACMLRCRQENPPLPLGSK 170  
 Db 121 RWYFDVERNSCNNF1YGGCRGNKNSYRSEACMLRCRQENPPLPLGSK 170  
 QY 121 RWYFDVERNSCNNF1YGGCRGNKNSYRSEACMLRCRQENPPLPLGSK 170  
 Db 121 RWYFDVERNSCNNF1YGGCRGNKNSYRSEACMLRCRQENPPLPLGSK 170

RESULT 11 AW30046	Db	61 CATTENATGDLATSRNAADSSVSPAPRQDSEDHSSDMNFNEYEYCTANAVTGPGRASFP 120
ID AAW30046 standard; Protein: 225 AA.	Qy	121 RWYFDVERNSCNNFIYGGCNGKNSYRSSEACMLHCFCRQENPPLGSK 170
XX	AC	
AAW30046;	XX	
XX	DB	121 RWYFDVERNSCNNFIYGGCNGKNSYRSSEACMLRCFRCQENPPLGSK 170
DT 20-APR-1998 (first entry)		
XX		
DE Human Placental bikunin.		
XX		
KW Human; placental bikunin; inhibition; trypsin; kallikrein;		
KW plasmin; factor XIIa; treatment; prevention; oedema;		
KW inflammation; infection; granulomatosis; multiple sclerosis;		
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;		
KW blood coagulation disease; polytrauma; stroke; haemorrhage;		
KW gastric cancer; cervical cancer; metastasis; blood loss.		
OS Homo sapiens.		
XX WO9733396-A2.		
XX PD 18-SEP-1997.		
XX PF 10-MAR-1997; 97WO-US03894.		
XX PR 04-OCT-1996; 96US-0725251.		
PR 11-MAR-1996; 96US-0013105.		
PR 14-JUN-1996; 96US-0019733.		
PA (FARB ) BAYER CORP.		
XX PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;		
XX DR WPI: 1997-470876/43.		
XX PT New human placental bikunin - used to inhibit kallikrein, trypsin		
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or		
PT perioperative blood loss.		
PS Claim 1; Page 66, 110pp; English.		
XX The present sequence is a human placental bikunin, which		
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.		
CC Bikunin can be used to treat or prevent brain and spinal cord		
CC oedema, inflammation, infection or granulomatosis, multiple		
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,		
CC fibrosis, blood coagulation diseases, polytrauma, stroke,		
CC cerebral or subarachnoid haemorrhage and gastric or cervical		
CC cancer and prevent metastasis. It is particularly useful for		
CC reducing blood loss during surgery, and can also be used to treat		
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,		
CC influenza and similar viral infections, acute pancreatitis and		
CC gout, and prevent pre-term labour. It has similar properties to		
CC aprotinin, but is less highly charged so should be less		
CC immunogenic and less likely to damage the kidneys. Manipulation		
CC of the bikunin sequence may allow the inhibitory profile to be		
CC altered. It also reduces or eliminates the need for whole donor		
CC blood or blood products during surgery, thereby reducing the risk		
CC of infection and other adverse side effects, as well as reducing		
CC the cost of surgery.		
XX Sequence 225 AA;		
Query Match 100.0%; Score 948; DB 18; Length 225;		
Best Local Similarity 100.0%; Pred. No. 5.7e-89; Mismatches 0; Indels 0; Gaps 0;		
Matches 170; Conservative 0; Gaps 0; Mismatches 0; Indels 0; Gaps 0;		
Qy 1 ADRESSTHDFFCLVSKVYGRCRASMPRWNWYNTDGSQQLFYGGCDGNSNNYLTKEECLKK 60		
DB 1 ADRESSTHDFFCLVSKVYGRCRASMPRWNWYNTDGSQQLFYGGCDGNSNNYLTKEECLKK 60		
Qy 61 CATTENATGDLATSRNAADSSVSPAPRQDSEDHSSDMNFNEYEYCTANAVTGPGRASFP 120		
SQ Sequence 225 AA;		
Query Match 100.0%; Score 948; DB 18; Length 225;		
Best Local Similarity 100.0%; Pred. No. 5.7e-89; Mismatches 0; Indels 0; Gaps 0;		
Matches 170; Conservative 0; Gaps 0; Mismatches 0; Indels 0; Gaps 0;		
Qy 1 ADRESSTHDFFCLVSKVYGRCRASMPRWNWYNTDGSQQLFYGGCDGNSNNYLTKEECLKK 60		
DB 1 ADRESSTHDFFCLVSKVYGRCRASMPRWNWYNTDGSQQLFYGGCDGNSNNYLTKEECLKK 60		

QY 61 CATTENATGDLATSRNAADSSVPSAPRQDSEDHSSDMENYEEYCTANAVTGPCRASFP 120  
 Db 61 CATTENATGDLATSRNAADSSVPSAPRQDSEDHSSDMENYEEYCTANAVTGPCRASFP 120  
 QY 121 RWYFDVERNSCNFNFYGGCRGKNSYSEACMLRCFRQENPPLPLGSK 170  
 Db 121 RWYFDVERNSCNFNFYGGCRGKNSYSEACMLRCFRQENPPLPLGSK 170

RESULT 13  
 AAB14201  
 ID AAB14201 standard; protein: 225 AA.  
 XX  
 AC AAB14201;  
 XX  
 DT 02-FEB-2001 (first entry)  
 DE Human placental bikunin protein fragment # 16.  
 XX  
 Human; mucociliary dysfunction; mucus; sputum;  
 KW chronic obstructive lung disease; chronic bronchitis; CB: Bronchiectasis;  
 BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;  
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.  
 XX  
 Homo sapiens.  
 OS Homo sapiens.  
 PN WO200037099-A2.  
 XX  
 PD 29-JUN-2000.  
 XX  
 PF 22-DEC-1999; 99WO-GB04381.  
 XX  
 PR 22-DEC-1998; 98US-0218913.  
 PR 17-NOV-1999; 98US-0441963.  
 XX  
 PA (FARB ) BAYER AG.  
 PI Hall R, Poll CT, Newton BB, Taylor WJA;  
 XX  
 DR WPI: 2000-452127/39.  
 XX  
 PR Stimulating mucociliary clearance rate of mucus and sputum in lung  
 PR airways for treating lung diseases such as cystic fibrosis and  
 PR bronchitis involves administering a Kunitz-type serine protease  
 PR inhibitor.  
 XX  
 PS Claim 13; Pages 88-89; 173pp; English.  
 CC Mucociliary dysfunction is the inability of ciliated epithelium to clear  
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious  
 CC complication of chronic obstructive lung diseases such as Chronic  
 CC Bronchitis (CB). Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).  
 CC In addition, patients suffering from mucociliary dysfunction are  
 CC susceptible to secondary bacterial infections. The present sequence is a  
 CC fragment of human placental bikunin. Human placental bikunin is a  
 CC Kunitz-type serine protease inhibitor protein, which can stimulate the  
 CC rate of mucociliary clearance of mucus and sputum in lung airways.  
 CC Therefore, the present protein fragment may be used for treating lung  
 CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are  
 CC caused by retention and accumulation of mucus.  
 XX  
 SQ Sequence 225 AA;

Query Match 100.0%; Score 948; DB 21; Length 225;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-89;  
 Matches 170; Conservative 0; Mismatches 0; Gaps 0;

QY 1 ADERSTHDFCLVSKVYGRCRASMPRQWYNTDGSQCLFYVGDDGNSNNYLTKEECLKK 60  
 1 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 1 AURERSTHDFCLVSKVYGRCRASMPRQWYNTDGSQCLFYVGDDGNSNNYLTKEECLKK 60  
 QY 61 CATTENATGDLATSRNAADSSVPSAPRQDSEDHSSDMENYEEYCTANAVTGPCRASFP 120  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 61 CATTENATGDLATSRNAADSSVPSAPRQDSEDHSSDMENYEEYCTANAVTGPCRASFP 120  
 QY 121 RWYFDVERNSCNFNFYGGCRGKNSYSEACMLRCFRQENPPLPLGSK 170  
 Db 121 RWYFDVERNSCNFNFYGGCRGKNSYSEACMLRCFRQENPPLPLGSK 170

RESULT 14  
 AAW30060  
 ID AAW30060 standard; Protein; 235 AA.  
 XX  
 AC AAW30060;  
 XX  
 DT 20-APR-1998 (first entry)  
 XX  
 DE Human consensus bikunin.  
 XX  
 Human; consensus bikunin; inhibition; trypsin; kallikrein;  
 KW plasmin; factor XIIa; treatment; prevention; oedema;  
 KW inflammation; infection; granulomatosis; multiple sclerosis;  
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;  
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;  
 KW gastric cancer; cervical cancer; metastasis; blood loss.  
 XX  
 Homo sapiens.  
 XX  
 Key Location/Qualifiers  
 FT Misc-difference 198  
 FT /note= "encoded by TGA"  
 FT Misc-difference 201  
 FT /note= "encoded by TGA"  
 FT Misc-difference 226  
 FT /note= "encoded by GAN"  
 FT Misc-difference 233  
 FT /note= "encoded by TGA"  
 XX  
 PN WO9733996-A2.  
 XX  
 PD 18-SEP-1997.  
 XX  
 PR 10-MAR-1997; 97WO-US03894.  
 XX  
 PR 04-OCT-1996; 96US-0725251.  
 PR 11-MAR-1996; 96US-0013106.  
 PR 14-JUN-1996; 96US-0019793.  
 XX  
 PA (FARB ) BAYER CORP.  
 XX  
 PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;  
 XX  
 DR WPI: 1997-470876/43.  
 DR N-PSDB; AAT90732.  
 XX  
 PT New human placental bikunin - used to inhibit kallikrein, trypsin  
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or  
 PT perioperative blood loss  
 XX  
 PS Disclosure; Fig 3; 110pp; English.  
 XX  
 The present sequence is a consensus human bikunin, which  
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.  
 CC Bikunin can be used to treat or prevent brain and spinal cord  
 CC oedema, inflammation, infection or granulomatosis, multiple  
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,  
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,  
 CC cerebral or subarachnoid haemorrhage and gastric or cervical  
 CC cancer and prevent metastasis. It is particularly useful for  
 CC reducing blood loss during surgery, and can also be used to treat  
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,  
 CC influenza and similar viral infections, acute pancreatitis and  
 CC gout, and prevent pre-term labour. It has similar properties to  
 CC aprotinin, but is less highly charged so should be less  
 CC immunogenic and less likely to damage the kidneys. Manipulation

of the bikunin sequence may allow the inhibitory profile to be altered. It also reduces or eliminates the need for whole donor blood or blood products during surgery, thereby reducing the risk of infection and other adverse side effects, as well as reducing the cost of surgery.

Homo sapiens.	Location/Qualifiers
key	
Misc-difference	198 /label= "unknown /note= "Encoded by TGA"
Misc-difference	201 /label= "unknown /note= "Encoded by TGA"
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Misc-difference	226 /label= "unknown /note= "Encoded by GAN"
Misc-difference	233 /label= "unknown /note= "Encoded by GAN"

WO2000037099-A2.  
29-JUN-2000.  
22-DEC-1999; 99WO-GB04381.  
22-DEC-1998; 98US-0218913.  
17-NOV-1999; 99US-0441966.  
(FARB ) BAYER AG.  
Hall R, Polli CT, Newton BB, Taylor WJA;  
WPI; 2000-452127/39.  
N-PSD; 2000-452127/39.

Stimulating mucociliary clearance rate of mucus and sputum in lung airways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease inhibitor - Disclosure; Fig 3; 173pp; English.

Mucociliary dysfunction is the inability of ciliated epithelium to clear mucus and sputum in lung airways. Mucociliary dysfunction is a serious complication of chronic obstructive lung diseases such as Chronic Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF). In addition, patients suffering from mucociliary dysfunction are susceptible to secondary bacterial infections. The present sequence is a human placental bikunin protein fragment. This protein is a Kunitz-type serine protease inhibitor protein, which can stimulate the rate of mucociliary clearance of mucus and sputum in lung airways. Therefore, the present sequence may be used for treating lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are caused by retention and accumulation of mucus.

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22-DEC-1999;	99WO-GB04381.			
22-DEC-1998;	98US-0218913.			
17-NOV-1999;	99US-0441966.			
(FARB ) BAYER AG.				
Hall R.	Poll CT,	Newton BB,	Taylor	
WPI: 2000-452127/39.				
N-NSNP. 2000-452127/39.				

